Package 'RJafroc'

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Description Analyzing the performance of artificial intelligence (AI) systems/algorithms characterized by a ``search-and-report'' strategy. While historically observer performance has dealt with measuring radiologists' performance in search tasks – i.e., searching for lesions in medical images and reporting them - the software described here applies equally to any task involving searching for and reporting arbitrary targets in images. The package can be used to analyze the performance of AI systems, compare AI performance to a group of human readers or optimize the reporting threshold of an AI system. In addition to performing conventional receiver operating characteristic (ROC) analysis (localization information ignored), the software also performs free-response receiver operating characteristic (FROC) analysis, where lesion localization information is integral to the analyzed data. A book using the software has been published: Chakraborty DP: Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples, Taylor-Francis LLC; 2017. An online update of this book is at <https://dpc10ster.github.io/RJafrocBook/>. Illustrations of the software (vignettes) are at <https://dpc10ster.github.io/RJafroc/>. Supported data collection paradigms are the ROC, FROC and the location ROC (LROC). ROC data consists of single ratings per images, where a rating is the perceived confidence level that the image is that of a diseased patient. An ROC curve is a plot of true positive fraction vs. false

positive fraction. FROC data consists of a variable number (zero or more) of mark-rating pairs per image, where a mark is the location of a reported suspicious region and the rating is the confidence level that it is a real lesion. LROC data consists of a rating and a location of the most suspicious region, for every image. Four models of observer performance, and curve-fitting software, are implemented: the binormal model (BM), the contaminated binormal model (CBM), the correlated contaminated binormal model (CORCBM), and the radiological search model (RSM). Unlike the binormal model, CBM, CORCBM and RSM predict ``proper'' ROC curves that do not inappropriately cross the chance diagonal. Additionally, RSM parameters are related to search performance (not measured in conventional ROC analysis) and classification performance.
Search performance refers to finding lesions, i.e., true positives, while simultaneously not finding false positive locations. Classification performance measures the ability to distinguish between true and false positive locations. Knowing these separate performances allows principled optimization of reader or AI system performance. RJafroc supersedes Windows JAFROC (jackknife alternative FROC) software V4.2.1, <https://github.com/dpc10ster/WindowsJafroc>. Package functions are organized as follows. Data file related function names are preceded by ``Df'', curve fitting functions by ``Fit'', included data sets by ``dataset'', plotting functions by ``Plot'', significance testing functions by ``St'', sample size related functions by ``Ss'', data simulation functions by ``Simulate'' and utility functions by ``Util''. Implemented are figures of merit (FOMs) for quantifying performance and functions for visualizing empirical or fitted operating characteristics: e.g., ROC, FROC, alternative FROC (AFROC) and weighted AFROC (wAFROC) curves. For fully crossed study designs significance testing of reader-averaged FOM differences between modalities is implemented via either Dorfman-Berbaum-Metz or the Obuchowski-Rockette methods. Also implemented is single treatment analysis, which allows comparison of performance of a group of radiologists to a specified value, or comparison of AI to a group of radiologists interpreting the same cases. Crossed-modality analysis is implemented wherein there are two crossed treatment factors and the aim is to determined performance in each treatment factor averaged over all levels of the second factor. Sample size estimation tools are provided for ROC and FROC studies; these use estimates of the relevant variances from a pilot study to predict required numbers of readers and cases in a pivotal study to achieve the desired power. Utility and data file manipulation functions allow data to be read in any of the currently used input formats, including Excel, and the results of the analysis can be viewed in text or Excel output files. The methods are

illustrated with several included datasets from the author's collaborations. This version corrects bugs, simplifies usage of
the software and updates the dataset structure. All changes are noted in NEWS.

License GPL-3

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Description

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curves. For fully crossed study designs significance testing of reader-averaged FOM differences between modalities is implemented via both Dorfman-Berbaum-Metz and the Obuchowski-Rockette methods. Also implemented are single treatment analyses, which allow comparison of performance of a group of radiologists to a specified value, or comparison of AI to a group of radiologists interpreting the same cases. Crossed-modality analysis is implemented wherein there are two crossed treatment factors and the aim is to determined performance in each treatment factor averaged over all levels of the second factor. Sample size estimation tools are provided for ROC and FROC studies; these use estimates of the relevant variances from a pilot study to predict required numbers of readers and cases in a pivotal study to achieve the desired power. Utility and data file manipulation functions allow data to be read in any of the currently used input formats, including Excel, and the results of the analysis can be viewed in text or Excel output files. The methods are illustrated with several included datasets from the author's collaborations. This version corrects bugs, simplifies usage of the software and updates the *dataset* structure. All changes are noted in NEWS.md.

Details

Package:	RJafroc
Type:	Package
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URL:	https://dpc10ster.github.io/RJafroc/

Definitions and abbreviations

- a: The separation or "a" parameter of the binormal model
- AFROC curve: plot of LLF (ordinate) vs. FPF, where FPF is inferred using highest rating of NL marks on **non-diseased cases**
- AFROC: alternative FROC, see Chakraborty 1989
- AFROC1 curve: plot of LLF (ordinate) vs. FPF1, where FPF1 is inferred using highest rating of NL marks on **ALL cases**
- $alpha$: The significance level α of the test of the null hypothesis of no treatment effect
- AUC: area under curve; e.g., ROC-AUC = area under ROC curve, an example of a FOM
- b: The width or "b" parameter of the conventional binormal model
- Binormal model: two unequal variance normal distributions, one at zero and one at mu, for modeling ROC ratings, $sigma$ is the std. dev. ratio of diseased to non-diseased distributions
- CAD: computer aided detection algorithm
- CBM: contaminated binormal model (CBM): two equal variance normal distributions for modeling ROC ratings, the diseased distribution is bimodal, with a peak at zero and one at μ, the integrated fraction at μ is α (not to be confused with α of NH testing)
- CI: The (1-α) confidence interval for the stated statistic

- Crossed modality: a dataset containing two modality (treatment) factors, with the levels of the two factors crossed, see paper by Thompson et al
- DBM: Dorfman-Berbaum-Metz, a significance testing method for detecting a treatment effect in MRMC studies
- DBMH: Hillis' modification of the DBM method
- ddf: Denominator degrees of freedom of appropriate F-test; the corresponding ndf is `I - 1`
- Empirical AUC: trapezoidal area under curve, same as the Wilcoxon statistic for ROC paradigm
- FN: false negative, a diseased case classified as non-diseased
- FOM: figure of merit, a quantitative measure of performance, performance metric
- FP: false positive, a non-diseased case classified as diseased
- FPF: number of FPs divided by number of non-diseased cases
- FROC curve: plot of LLF (ordinate) vs. NLF
- FROC: free-response ROC (a data collection paradigm where each image yields a random number, 0, 1, 2,..., of mark-rating pairs)
- FRRC: Analysis that treats readers as fixed and cases as random factors
- I: total number of modalities, indexed by i
- image/case: used interchangeably; a case can consist of several images of the same patient in the same treatment
- iMRMC: A text file format used for ROC data by FDA/CDRH researchers
- individual: A single-treatment single-reader dataset.
- Intrinsic: Used in connection with RSM; a parameter that is independent of the RSM μ parameter, but whose meaning may not be as transparent as the corresponding physical parameter
- J: number of readers, indexed by `j`
- JAFROC file format: A .xlsx format file, applicable to ROC, ROI, FROC and LROC paradigms
- JAFROC: jackknife AFROC: Windows software for analyzing observer performance data: no longer updated, replaced by current package; the name is a misnomer as the jackknife is used only for significance testing; alternatively, the bootstrap could be used; what distinguishes FROC from ROC analysis is the use of the AFROC-AUC as the FOM. With this change, the DBM or the OR method can be used for significance testing
- `K`: total number of cases, `K = K1 + K2`, indexed by k
- `K1`: total number of non-diseased cases, indexed by $k1$
- `K2`: total number of diseased cases, indexed by $k2$
- LL: lesion localization i.e., a mark that correctly locates an existing localized lesion; TP is a special case, when the proximity criterion is lax (i.e., "acceptance radius" is large)
- LLF: number of LLs divided by the total number of lesions
- LROC: location receiver operating characteristic, a data collection paradigm where each image yields a single rating and one location
- lrc/MRMC: A text file format used for ROC data by University of Iowa researchers
- mark: the location of a suspected diseased region
- maxLL: maximum number of lesions per case in dataset

- maxNL: maximum number of NL marks per case in dataset
- MRMC: multiple reader multiple case (each reader interprets each case in each treatment, i.e. fully crossed study design)
- ndf: Numerator degrees of freedom of appropriate F-test, usually number of treatments minus one
- NH: The null hypothesis that all treatment effects are zero; rejected if the p-value is smaller than α
- NL: non-lesion localization, of which FP is a special case, i.e., a mark that does not correctly locate any existing localized lesion(s)
- NLF: number of NLs divided by the total number of cases
- Operating characteristic: A plot of normalized correct decisions on diseased cases along ordinate vs. normalized incorrect decisions on non-diseased cases
- Operating point: A point on an operating characteristic, e.g., (FPF, TPF) represents an operating point on an ROC
- OR: Obuchowski-Rockette, a significance testing method for detecting a treatment effect in MRMC studies
- ORH: Hillis' modification of the OR method
- Physical parameter: Used in connection with RSM; a parameter whose meaning is more transparent than the corresponding intrinsic parameter, but which depends on the RSM μ parameter
- Proximity criterion / acceptance radius: Used in connection with FROC (or LROC data); the "nearness" criterion is used to determine if a mark is close enough to a lesion to be counted as a LL (or correct localization); otherwise it is counted as a NL (or incorrect localization)
- p-value: the probability, under the null hypothesis, that the observed treatment effects, or larger, could occur by chance
- Proper: a proper fit does not inappropriately fall below the chance diagonal, does not display a "hook" near the upper right corner
- PROPROC: Metz's binormal model based fitting of proper ROC curves
- RSM, Radiological Search Model: two unit variance normal distributions for modeling NL and LL ratings; four parameters, μ, ν', λ' and $\zeta 1$
- Rating: Confidence level assigned to a case; higher values indicate greater confidence in presence of disease; `-Inf` is allowed but `NA` is not allowed
- Reader/observer/radiologist/CAD: used interchangeably
- RJafroc: the current software
- ROC: receiver operating characteristic, a data collection paradigm where each image yields a single rating and location information is ignored
- ROC curve: plot of TPF (ordinate) vs. FPF, as threshold is varied; an example of an operating characteristic
- ROCFIT: Metz software for binormal model based fitting of ROC data
- ROI: region-of-interest (each case is divided into a number of ROIs and the reader assigns an ROC rating to each ROI)
- FRRC: Analysis that treats readers as fixed and cases as random factors

- RRFC: Analysis that treats readers as random and cases as fixed factors
- RRRC: Analysis that treats both readers and cases as random factors
- RSCORE-II: original software for binormal model based fitting of ROC data
- RSM: Radiological search model, also method for fitting a proper ROC curve to ROC data
- RSM-ζ1: Lowest reporting threshold, determines if suspicious region is actually marked
- RSM-λ: Intrinsic parameter of RSM corresponding to λ', independent of μ
- RSM-λ': Physical Poisson parameter of RSM, average number of latent NLs per case; depends on μ
- RSM-μ: separation of the unit variance distributions of RSM
- RSM-ν: Intrinsic parameter of RSM, corresponding to ν', independent of μ
- RSM-ν': binomial parameter of RSM, probability that lesion is found
- SE: sensitivity, same as TPF
- Significance testing: determining the p-value of a statistical test
- SP: specificity, same as $1 - FPF$
- Threshold: Reporting criteria: if confidence exceeds a threshold value, report case as diseased, otherwise report non-diseased
- TN: true negative, a non-diseased case classified as non-diseased
- TP: true positive, a diseased case classified as diseased
- TPF: number of TPs divided by number of diseased cases
- Treatment/modality: used interchangeably, for example, computed tomography (CT) images vs. magnetic resonance imaging (MRI) images
- wAFROC curve: plot of weighted LLF (ordinate) vs. FPF, where FPF is inferred using highest rating of NL marks on **non-diseased cases ONLY**
- wAFROC1 curve: plot of weighted LLF (ordinate) vs. FPF1, where FPF1 is inferred using highest rating of NL marks on **ALL cases**
- wAFROC1 FOM: weighted trapezoidal area under AFROC1 curve: only use if there are zero non-diseased cases is always number of treatments minus one

Dataset

The `dataset` object has 3 `list` elements: `$ratings`, `$lesions` and `$descriptions`, where:

- `dataset$ratings`: contains 3 elements as sub-lists: `$NL`, `$LL` and `$LL_IL`; these describe the structure of the ratings;
- `dataset$lesions`: contains 3 elements as sub-lists: `$perCase`, `$IDs` and `$weights`; these describe the structure of the lesions;
- `dataset$descriptions`: contains 7 elements as sub-lists: `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID`; these describe other characterisitcs of the dataset as detailed next.

Note: `-Inf` **is used to indicate the ratings of unmarked lesions and/or missing values.** As an example of the latter, if the maximum number of NLs in a dataset is 4, but some images have fewer than 4 NL marks, the corresponding "empty" positions would be filled with `-Infs`. **Do not use** `NA` **to denote a missing rating.**

Note: **"dataset" in this package always represents** `R` **object(s) with the following structure(s):**

General data structure, e.g., `dataset02`**, an ROC dataset, and** `dataset05`**, an FROC dataset.:**

- `ratings$NL`: a float array with dimensions `c(I,J,K,maxNL)`, containing the ratings of NL marks. The first `K1` locations of the third index corresponds to NL marks on non-diseased cases and the remaining locations correspond to NL marks on diseased cases. The 4th dimension allows for multiple NL marks on a case: the first index holds the first NL rating on the image, the second holds the second NL rating on the image, etc. The value of `maxNL` is determined by the case with the maximum number of lesions per case in the dataset. For **FROC** datasets missing NL ratings are assigned the `-Inf` rating. For **ROC** datasets, FP ratings are assigned to the first `K1` elements of `NL[,,1:K1,1]` and the remaining `K2` elements of `NL[,,(K1+1):K,1]` are set to `-Inf`.
- `ratings$LL`: for non-LROC datasets a float array with dimensions `c(I,J,K2,maxLL)` containing the ratings of LL marks. The value of `maxLL` is determined by the maximum number of lesions per case in the dataset. Unmarked lesions are assigned the `-Inf` rating. For ROC datasets `TP` ratings are assigned to `LL[,,1:K2,1]`. For **LROC** datasets it is a float array with dimensions `c(I,J,K2,1)` containing the ratings of correct localizations, otherwise the rating is recorded in the incorrect localization array described next.
- `ratings$LL_IL`: for LROC datasets the ratings of incorrect localization marks on abnormal cases. It is a float array with dimensions `c(I,J,K2,1)`. For non-LROC datasets this array is filled with NAs.
- `lesions$perCase`: an integer array with length `K2`, the number of lesions on each diseased case. The maximum value of this array equals `maxLL`. For example, `dataset05$lesions$perCase[4` is 2, meaning the 4th diseased case has two lesions.
- `lesions$IDs`: an integer array with dimensions `[K2, maxLL]`, labeling (or naming) the lesions on the diseased cases. For example, `dataset05$lesions$IDs[4,]` is `c(1,2,-Inf)`, meaning the 4th diseased case has two lesions, labeled 1 and 2.
- `lesions$weights`: a floating point array with dimensions `c(K2,maxLL)`, representing the relative importance of detecting each lesion. The weights for an abnormal case must sum to unity. For example, `dataset05$lesions$weights[4,]` is `c(0.5,0.5,-Inf)`, corresponding to equal weights (0.5) assigned to of the two lesions in the case.
- `descriptions$fileName`: a `character` variable containing the file name of the source data for this dataset. This is generated automatically by the DfReadDataFile function used to read the file. For a simulalated dataset it is set to "NA" (i.e., a character vector, not the variable `NA`).
- `descriptions$type`: a `character` variable describing the data type: `"ROC"`, `"LROC"`, `"ROI"` or `"FROC"`.
- `descriptions$name`: a `character` variable containing the name of the dataset: e.g., "dataset02" or "dataset05". This is generated automatically by the DfReadDataFile function used to read the file.
- `descriptions$truthTableStr`: a `c(I,J,L,maxLL+1)` object. For normal cases elements `c(I,J,L,1)` are filled with 1s if the corresponding interpretations occurred or NAs otherwise. For abnormal cases elements `c(I,J,L,2:(maxLL+1))` are filled with 1s if the corre-

sponding interpretations occurred or NAs otherwise. This object is necessary for analyzing more complex designs, e.g., split-plot, as described next.

- `descriptions$design`: a `character` variable: `"FCTRL"`, `"SPLIT-PLOT-A"` or `"SPLIT-PLOT-A"`, corresponding to factorial, split-plot-A or split-plot-C designs. The A and C refer to subparts of Table VII in a Hillis 2014 publication.
- `descriptions$modalityID`: a `character` vector of length I, which labels/names the modalities in the dataset.
- `descriptions$readerID`: a `character` vector of length J, which labels/names the readers in the dataset.

ROI data structure, example `datasetROI`**:** Only changes from the previously described structure are described below:

- `ratings$NL`: a float array with dimensions `c(I,J,K,Q)` containing the ratings of each of Q quadrants for each non-diseased case.
- `ratings$LL`: a float array with dimensions `c(I,J,K2,Q)` containing the ratings of quadrants for each diseased case.
- `lesions$perCase`: this contains the locations, on abnormal cases, containing at least one lesion.

Crossed modality data structure, example `datasetCrossedModality`**:** Only changes from the previously described structure are described below:

- `ratings$NL`: a float array with dimension `c(I1,I2,J,K,maxNL)` containing the ratings of NL marks. Note the existence of two modality indices.
- `LL`: a float array with dimension `c(I1,I2,J,K2,maxLL)` containing the ratings of all LL marks. Note the existence of two modality indices.
- `modalityID1`: corresponding to first modality factor.
- `modalityID2`: corresponding to second modality factor.

Df: Datafile Related Functions

- `Df2RJafrocDataset`: Convert a ratings array to a dataset object.
- `DfBinDataset`: Return a binned dataset.
- `DfCreateCorCbmDataset`:Create paired dataset for testing FitCorCbm.
- `DfExtractDataset`: Extract a subset of modalities and readers from a dataset.
- `DfFroc2Roc`: Convert an FROC dataset to a highest rating inferred ROC dataset.
- `DfLroc2Roc`: Convert an LROC dataset to a highest rating inferred ROC dataset.
- `DfLroc2Froc`: Simulates an "AUC-equivalent" FROC dataset from a supplied LROC dataset.
- `DfFroc2Lroc`: Simulates an "AUC-equivalent" LROC dataset from a supplied FROC dataset.
- `DfReadCrossedModalities`: Read a crossed-modalities data file.
- `DfReadDataFile`: Read a general data file.
- `DfSaveDataFile`: Save ROC data file in a different format.
- `DfExtractCorCbmDataset`: Extract two arms of a pairing from an MRMC ROC dataset suitable for using FitCorCbm.

Fitting Functions

- FitBinormalRoc: Fit the binormal model to ROC data (R equivalent of ROCFIT or RSCORE).
- FitCbmRoc: Fit the contaminated binormal model (CBM) to ROC data.
- FitRsmRoc: Fit the radiological search model (RSM) to ROC data.
- FitCorCbm: Fit the correlated contaminated binormal model (CORCBM) to paired ROC data.
- FitRsmRoc: Fit the radiological search model (RSM) to ROC data.

Plotting Functions

- PlotBinormalFit: Plot binormal-predicted ROC curve with provided BM parameters.
- PlotEmpiricalOperatingCharacteristics: Plot empirical operating characteristics for specified dataset.
- PlotRsmOperatingCharacteristics: Plot RSM-fitted ROC curves.

Simulation Functions

- SimulateFrocDataset: Simulates an uncorrelated FROC dataset using the RSM.
- SimulateRocDataset: Simulates an uncorrelated binormal model ROC dataset.
- SimulateCorCbmDataset: Simulates an uncorrelated binormal model ROC dataset.
- SimulateLrocDataset: Simulates an uncorrelated LROC dataset.

Sample size Functions

- SsPowerGivenJK: Calculate statistical power given numbers of readers J and cases K.
- SsPowerTable: Generate a power table.
- SsSampleSizeKGivenJ: Calculate number of cases K, for specified number of readers J, to achieve desired power for an ROC study.

Significance Testing Functions

- StSignificanceTesting: Perform significance testing, DBM or OR.
- StSignificanceTestingCadVsRad: Perform significance testing, CAD vs. radiologists.
- StSignificanceTestingCrossedModalities: Perform significance testing using crossed modalities analysis.

Miscellaneous and Utility Functions

- Compare3ProperRocFits: Compare three proper-ROC curve fitting models.
- UtilAucBinormal: Binormal model AUC function.
- UtilAucCBM: CBM AUC function.
- UtilAucPROPROC: PROPROC AUC function.
- UtilAnalyticalAucsRSM: RSM ROC/AFROC AUC calculator.
- UtilFigureOfMerit: Calculate empirical figures of merit (FOMs) for specified dataset.

- UtilIntrinsic2PhysicalRSM: Convert from intrinsic to physical RSM parameters.
- UtilLesionDistr: Calculates the lesion distribution matrix.
- UtilLesionWeightsDistr: Calculates the lesion weights matrix.
- UtilMeanSquares: Calculates the mean squares used in the DBMH and ORH methods.
- UtilOutputReport: Generate a formatted report file.
- UtilPhysical2IntrinsicRSM: Convert from physical to intrinsic RSM parameters.
- UtilPseudoValues: Return jackknife pseudovalues.
- UtilVarComponentsDBM: Utility for Dorfman-Berbaum-Metz variance components.
- UtilORVarComponentsFactorial: Utility for Obuchowski-Rockette variance components.

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Zhai X, Chakraborty DP. (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. doi: 10.1002/mp.12263:2207–2222.

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Chakraborty DP, Nishikawa RM, Orton CG. Due to potential concerns of bias and conflicts of interest, regulatory bodies should not do evaluation methodology research related to their regulatory missions. Medical Physics. 2017.

Dobbins III JT, McAdams HP, Sabol JM, Chakraborty DP, et al. (2016) Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 282(1):236-250.

Warren LM, Mackenzie A, Cooke J, et al. Effect of image quality on calcification detection in digital mammography. Medical Physics. 2012;39(6):3202-3213.

Chakraborty DP, Zhai X. On the meaning of the weighted alternative free-response operating characteristic figure of merit. Medical physics. 2016;43(5):2548-2557.

Chakraborty DP. (2017) Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples. Taylor-Francis, LLC.

`ChisqrGoodnessOfFit` *Compute the chisquare goodness of fit statistic for ROC fitting model*

Description

Compute the chisquare goodness of fit statistic for specified ROC data fitting model

Usage

```
ChisqrGoodnessOfFit(fpCounts, tpCounts, parameters, model, lesDistr)
```

Arguments

`fpCounts`	The FP counts table
`tpCounts`	The TP counts table
`parameters`	The parameters of the model including cutoffs, see details
`model`	The fitting model: "BINORMAL", "CBM" or "RSM
`lesDistr`	The lesion distribution matrix; not needed for "BINORMAL" or "CBM" models. Array [1:maxLL,1:2]. The probability mass function of the lesion distribution for diseased cases. The first column contains the actual numbers of lesions per case. The second column contains the fraction of diseased cases with the number of lesions specified in the first column. The second column must sum to unity.

Details

For model = "BINORMAL" the parameters are c(a,b,zetas). For model = "CBM" the parameters are c(mu,alpha,zetas). For model = "RSM" the parameters are c(mu,lambdaP,nuP,zetas).

Value

The return value is a list with the following elements:

`chisq`	The chi-square statistic
`pVal`	The p-value of the fit
`df`	The degrees of freedom

`Compare3ProperRocFits` *Compare three proper-ROC curve fitting models*

Description

Applies the Radiological Search Model (RSM) and the Contaminated Binormal Model (CBM) ROC-curve fitting methods to 14 datasets and compares the fits to Proper ROC (PROPROC) fits obtained using Windows software downloaded from the Univ. of Iowa ROC website ca. June 2017.

Usage

```
Compare3ProperRocFits(
  startIndx = 1,
  endIndx = 14,
  showPlot = FALSE,
  saveProprocLrcFile = FALSE,
  reAnalyze = FALSE
)
```

Arguments

`startIndx`	An integer in the range 1 to 14.
`endIndx`	An integer in the range 1 to 14, greater than or equal to `startIndx`.
`showPlot`	If `TRUE` the three plots are shown along with 95 percent confidence intervals on the lowest and uppermost operating points. The default is `FALSE`.
`saveProprocLrcFile`	If `TRUE` the binned datasets are saved for subsequent analysis using other ROC software, e.g., Windows DBM-MRMC. The default is `FALSE`.
`reAnalyze`	If `TRUE` the data is reanalyzed. The default is `FALSE` in which case the previously saved results are used.

Details

allDatasetsResults is a list-array of length (`endIndx - startIndx + 1`), where each element of the list-array is a list with 10 elements.

- `allDatasetsResults[[1]][[1]]`parameters of treatment 1 reader 1 in dataset `startIndx`
- `allDatasetsResults[[1]][[2]]`parameters of treatment 1 reader 2 in dataset `startIndx`
- `allDatasetsResults[[1]][[IJ]]`parameters of treatment `I` reader `J` in dataset `startIndx`
- `allDatasetsResults[[2]][[1]]`parameters of treatment 1 reader 1 in dataset `startIndx+1`
- `allDatasetsResults[[2]][[2]]`parameters of treatment 1 reader 2 in dataset `startIndx+1`
- `allDatasetsResults[[2]][[IJ]]`parameters of treatment `I` reader `J` in dataset `startIndx+1`
- `allBinnedDatasets[[1]]`binned ROC dataset corresponding to dataset `startIndx`
- `allDatasetsResults[[2]][[IJ]]`binned ROC dataset corresponding to dataset `startIndx+1`

A specific member, e.g., `allDatasetsResults[[1]][[1]]`, has the following structure:

- `retRsm` The RSM parameters following the output structure of `FitRsmRoc`
- `retCbm` The CBM parameters following the output structure of `FitCbmRoc`
- `lesDistr` The lesion distribution matrix
- `c1` The c-parameter of PROPROC
- `da` The `d_sub_a` parameter of PROPROC
- `aucProp` The `PROPROC` AUC
- `I` The number of treatments
- `J` The number of readers
- `K1` The number of non-diseased cases
- `K2` The number of diseased cases

The PROPROC parameters were obtained by running Windows software OR DBM-MRMC 2.50 (Sept. 04, 2014, Build 4) with **PROPROC** and **area** selected. The `RSM` and `CBM` fits are implemented in this package. Chapter 19 of the author's book has further details. If `saveProprocLrcFile` is `TRUE`, the `.lrc` files will be written to the `inst-MRMCRuns` directory, to appropriate subdirectory, **overwriting** any existing files.

Value

The returned value is a list of 2: `allDatasetsResults` containing the fitting results and `allBinnedDatasets` containing the binned datasets used in the fitting. See details.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Metz CE, Pan X 1999 Proper Binormal ROC Curves: Theory and Maximum-Likelihood Estimation. J Math Psychol. **43**,(1):1–33.

Dorfman DD, Berbaum KS, 2000 A contaminated binormal model for ROC data: Part II. A formal model Acad Radiol **7**, 427–437.

Examples

```
ret <- Compare3ProperRocFits(1,1) # analyze first two datasets


## takes longer than 5 sec on OSX
## ret <- Compare3ProperRocFits(1,2,reAnalyze = TRUE) # analyze first two datasets
## x <- ret$allDatasetsResults
## str(x[[1]][[1]]) # parameters for dataset 1 trt 1 and rdr 1
## str(x[[1]][[2]]) # parameters for dataset 1 trt 1 and rdr 2
## str(x[[1]][[10]])# parameters for dataset 1 trt 2 and rdr 5
## str(x[[2]][[1]]) # parameters for dataset 2 trt 1 and rdr 1
## str(x[[2]][[2]]) # parameters for dataset 2 trt 1 and rdr 2
## str(x[[2]][[10]])# parameters for dataset 2 trt 2 and rdr 5
```

```
## these examples will cause errors;
##these are intended to illustrate the structure of the functions return object
## str(x[[1]][[11]])# error
## str(x[[3]][[1]]) # error
```

`dataset01` *TONY FROC dataset*

Description

This is referred to in the book as the "TONY" dataset. It consists of 185 cases, 89 of which are diseased, interpreted in two treatments ("BT" = breast tomosynthesis and "DM" = digital mammography) by five radiologists using the FROC paradigm.

Usage

```
dataset01
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:2, 1:5, 1:185, 1:3], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:2, 1:5, 1:89, 1:2], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:89], number of lesions per diseased case
- `lesions$IDs`, num [1:89, 1:2], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:89, 1:2], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset01", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "FROC", the data type
- `descriptions$name`, chr "TONY", the name of the dataset
- `descriptions$truthTableStr`, num [1:2, 1:5, 1:185, 1:4] 1 1 1 1 ..., truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:2] "BT" "DM", treatment labels
- `descriptions$readerID`, chr [1:5] "1" "2" "3" "4" ..., reader labels

References

Chakraborty DP, Svahn T (2011) Estimating the parameters of a model of visual search from ROC data: an alternate method for fitting proper ROC curves. PROC SPIE 7966.

Examples

```
str(dataset01)
PlotEmpiricalOperatingCharacteristics(dataset = dataset01, opChType = "wAFROC")$Plot
```

`dataset02` *Van Dyke ROC dataset*

Description

This is referred to in the book as the "VD" dataset. It consists of 114 cases, 45 of which are diseased, interpreted in two treatments ("0" = single spin echo MRI, "1" = cine-MRI) by five radiologists using the ROC paradigm. Each diseased cases had an aortic dissection; the ROC paradigm generates one rating per case. Often referred to in the ROC literature as the Van Dyke dataset, which, along with the Franken dataset, has been widely used to illustrate advances in ROC methodology. The example below displays the ROC plot for the first treatment and first reader.

Usage

```
dataset02
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:2, 1:5, 1:114, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:2, 1:5, 1:45, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:45], number of lesions per diseased case
- `lesions$IDs`, num [1:45, 1], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:45, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset02", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "VAN-DYKE", the name of the dataset
- `descriptions$truthTableStr`, num [1:2, 1:5, 1:114, 1:2] 1 1 1 1 ..., truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:2] "0" "1", treatment labels
- `descriptions$readerID`, chr [1:5] "0" "1" "2" ..., reader labels

References

Van Dyke CW, et al. Cine MRI in the diagnosis of thoracic aortic dissection. 79th RSNA Meetings. 1993.

Examples

```
str(dataset02)
PlotEmpiricalOperatingCharacteristics(dataset = dataset02, opChType = "ROC")$Plot
```

`dataset03` *Franken ROC dataset*

Description

This is referred to in the book as the "FR" dataset. It consists of 100 cases, 67 of which are diseased, interpreted in two treatments, "0" = conventional film radiographs, "1" = digitized images viewed on monitors, by four radiologists using the ROC paradigm. Often referred to in the ROC literature as the Franken-dataset, which, along the the Van Dyke dataset, has been widely used to illustrate advances in ROC methodology.

Usage

```
dataset03
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:2, 1:4, 1:100, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:2, 1:4, 1:67, 1], ratings of lesion localizations, LLs
- `rating$LL_ILNA`, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:67], number of lesions per diseased case
- `lesions$IDs`, num [1:67, 1], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:67, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset03", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "FRANKEN", the name of the dataset
- `descriptions$truthTableStr`, num [1:2, 1:4, 1:100, 1:2], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset

- descriptions$modalityID, chr [1:2] "TREAT1" "TREAT2", treatment labels
- descriptions$readerID, chr chr [1:4] "READER_1" "READER_2" "READER_3" "READER_4", reader labels

References

Franken EA, et al. Evaluation of a Digital Workstation for Interpreting Neonatal Examinations: A Receiver Operating Characteristic Study. Investigative Radiology. 1992;27(9):732-737.

Examples

```
str(dataset03)
PlotEmpiricalOperatingCharacteristics(dataset = dataset03, opChType = "ROC")$Plot
```

---

dataset04 *Federica Zanca FROC dataset*

Description

This is referred to in the book as the "FED" dataset. It consists of 200 mammograms, 100 of which contained one to 3 simulated microcalcifications, interpreted in five treatments (basically different image processing algorithms) by four radiologists using the FROC paradigm and a 5-point rating scale. The maximum number of NLs per case, over the entire dataset was 7 and the dataset contained at least one diseased mammogram with 3 lesions. The Excel file containing this dataset is /inst/extdata/datasets/FZ_ALL.xlsx. The normal cases are labeled 100:199 while the normal cases are labeled 0:99.

Usage

```
dataset04
```

Format

A list with 3 elements: $ratings, $lesions and $descriptions; $ratings contain 3 elements, $NL, $LL and $LL_IL as sub-lists; $lesions contain 3 elements, $perCase, $IDs and $weights as sub-lists; $descriptions contain 7 elements, $fileName, $type, $name, $truthTableStr, $design, $modalityID and $readerID as sub-lists;

- rating$NL, num [1:5, 1:4, 1:200, 1:7], ratings of non-lesion localizations, NLs
- rating$LL, num [1:5, 1:4, 1:100, 1:3], ratings of lesion localizations, LLs
- rating$LL_ILNA, this placeholder is used only for LROC data
- lesions$perCase, int [1:100], number of lesions per diseased case
- lesions$IDs, num [1:100, 1:3], numeric labels of lesions on diseased cases
- lesions$weights, num [1:100, 1:3], weights (or clinical importances) of lesions

- descriptions$fileName, chr, "dataset04", base name of dataset in ‘data‘ folder
- descriptions$type, chr "FROC", the data type
- descriptions$name, chr "FEDERICA", the name of the dataset
- descriptions$truthTableStr, num [1:5, 1:4, 1:200, 1:4], truth table structure
- descriptions$design, chr "FCTRL", study design, factorial dataset
- descriptions$modalityID, chr [1:5] "1" "2" "3" "4" "5", treatment labels
- descriptions$readerID, chr [1:4] "1" "3" "4" "5", reader labels

References

Zanca F et al. Evaluation of clinical image processing algorithms used in digital mammography. Medical Physics. 2009;36(3):765-775.

Examples

```
str(dataset04)
PlotEmpiricalOperatingCharacteristics(dataset = dataset04, opChType = "wAFROC")$Plot
```

---

dataset05 *John Thompson FROC dataset*

Description

This is referred to in the book as the "JT" dataset. It consists of 92 cases, 47 of which are diseased, interpreted in two treatments ("1" = CT images acquired for attenuation correction, "2" = diagnostic CT images), by nine radiographers using the FROC paradigm. Each case was a slice of an anthropomorphic phantom 47 with inserted nodular lesions (max 3 per slice). The maximum number of NLs per case, over the entire dataset was 7.

Usage

```
dataset05
```

Format

A list with 3 elements: $ratings, $lesions and $descriptions; $ratings contain 3 elements, $NL, $LL and $LL_IL as sub-lists; $lesions contain 3 elements, $perCase, $IDs and $weights as sub-lists; $descriptions contain 7 elements, $fileName, $type, $name, $truthTableStr, $design, $modalityID and $readerID as sub-lists;

- rating$NL, num [1:2, 1:9, 1:92, 1:7], ratings of non-lesion localizations, NLs
- rating$LL, num [1:2, 1:9, 1:47, 1:3], ratings of lesion localizations, LLs
- rating$LL_ILNA, this placeholder is used only for LROC data

- lesions$perCase, int [1:47], number of lesions per diseased case
- lesions$IDs, num [1:47, 1:3], numeric labels of lesions on diseased cases
- lesions$weights, num [1:47, 1:3], weights (or clinical importances) of lesions
- descriptions$fileName, chr, "dataset05", base name of dataset in ‘data‘ folder
- descriptions$type, chr "FROC", the data type
- descriptions$name, chr "THOMPSON", the name of the dataset
- descriptions$truthTableStr, num [1:2, 1:9, 1:92, 1:4], truth table structure
- descriptions$design, chr "FCTRL", study design, factorial dataset
- descriptions$modalityID, chr [1:2] "1" "2", treatment labels
- descriptions$readerID, chr [1:4] "1" "2" "3" "4", reader labels

References

Thompson JD et al. Effect of reconstruction methods and x-ray tube current-time product on nodule detection in an anthropomorphic thorax phantom: a crossed-treatment JAFROC observer study. Medical Physics. 2016;43(3):1265-1274.

Examples

```
str(dataset05)
PlotEmpiricalOperatingCharacteristics(dataset = dataset05, opChType = "wAFROC")$Plot
```

---

dataset06 *Magnus FROC dataset*

Description

This is referred to in the book as the "MAG" dataset (after Magnus Bath, who conducted the JAFROC analysis). It consists of 100 cases, 69 of which are diseased, interpreted in two treatments ("1" = conventional chest, "1" = chest tomosynthesis) by four radiologists using the FROC paradigm.

Usage

```
dataset06
```

Format

A list with 3 elements: $ratings, $lesions and $descriptions; $ratings contain 3 elements, $NL, $LL and $LL_IL as sub-lists; $lesions contain 3 elements, $perCase, $IDs and $weights as sub-lists; $descriptions contain 7 elements, $fileName, $type, $name, $truthTableStr, $design, $modalityID and $readerID as sub-lists;

- rating$NL, num [1:2, 1:4, 1:89, 1:17], ratings of non-lesion localizations, NLs
- rating$LL, num [1:2, 1:4, 1:42, 1:15], ratings of lesion localizations, LLs
- rating$LL_ILNA, this placeholder is used only for LROC data
- lesions$perCase, int [1:42], number of lesions per diseased case
- lesions$IDs, num [1:42, 1:15], numeric labels of lesions on diseased cases
- lesions$weights, num [1:42, 1:15], weights (or clinical importances) of lesions
- descriptions$fileName, chr, "dataset06", base name of dataset in ‘data‘ folder
- descriptions$type, chr "FROC", the data type
- descriptions$name, chr "MAGNUS", the name of the dataset
- descriptions$truthTableStr, num [1:2, 1:4, 1:89, 1:16], truth table structure
- descriptions$design, chr "FCTRL", study design, factorial dataset
- descriptions$modalityID, chr [1:2] "1" "2", treatment labels
- descriptions$readerID, chr [1:4] "1" "2" "3" "4", reader labels

References

Vikgren J et al. Comparison of Chest Tomosynthesis and Chest Radiography for Detection of Pulmonary Nodules: Human Observer Study of Clinical Cases. Radiology. 2008;249(3):1034-1041.

Examples

```
str(dataset06)
PlotEmpiricalOperatingCharacteristics(dataset = dataset06, opChType = "wAFROC")$Plot
```

---

dataset07 *Lucy Warren FROC dataset*

Description

This is referred to in the book as the "OPT" dataset (for OptiMam). It consists of 162 cases, 81 of which are diseased, interpreted in five treatments (see reference, basically different ways of acquiring the images) by seven radiologists using the FROC paradigm.

Usage

```
dataset07
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:5, 1:7, 1:162, 1:4], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:5, 1:7, 1:81, 1:3], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:81], number of lesions per diseased case
- `lesions$IDs`, num [1:81, 1:3], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:81, 1:3], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset07", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "FROC", the data type
- `descriptions$name`, chr "LUCY-WARREN", the name of the dataset
- `descriptions$truthTableStr`, num [1:5, 1:7, 1:162, 1:4], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, [1:5] "1" "2" "3" "4" ..., treatment labels
- `descriptions$readerID`, chr [1:7] "1" "2" "3" "4" ..., reader labels

References

Warren LM, Mackenzie A, Cooke J, et al. Effect of image quality on calcification detection in digital mammography. Medical Physics. 2012;39(6):3202-3213.

Examples

```
str(dataset07)
PlotEmpiricalOperatingCharacteristics(dataset = dataset07, opChType = "wAFROC")$Plot
```

---

dataset08 *Monica Penedo ROC dataset*

Description

This is referred to in the book as the "PEN" dataset. It consists of 112 cases, 64 of which are diseased, interpreted in five treatments (basically different image compression algorithms) by five radiologists using the FROC paradigm (the inferred ROC dataset is included; the original FROC data is lost).

Usage

```
dataset08
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:5, 1:5, 1:112, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:5, 1:5, 1:64, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:64], number of lesions per diseased case
- `lesions$IDs`, num [1:64, 1], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:64, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset08", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "PENEDO", the name of the dataset
- `descriptions$truthTableStr`, num [1:5, 1:5, 1:112, 1:2], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:5] "0" "1" "2" "3" ..., treatment labels
- `descriptions$readerID`, chr [1:5] "0" "1" "2" "3" ..., reader labels

References

Penedo et al. Free-Response Receiver Operating Characteristic Evaluation of Lossy JPEG2000 and Object-based Set Partitioning in Hierarchical Trees Compression of Digitized Mammograms. Radiology. 2005;237(2):450-457.

Examples

```
str(dataset08)
PlotEmpiricalOperatingCharacteristics(dataset = dataset08, opChType = "ROC")$Plot
```

`dataset09` *Nico Karssemeijer ROC dataset (CAD vs. radiologists)*

Description

This is referred to in the book as the "NICO" dataset. It consists of 200 mammograms, 80 of which contain one malignant mass, interpreted by a CAD system and nine radiologists using the LROC paradigm. The first reader is CAD. The highest rating was used to convert this to an ROC dataset. The original LROC data is `datasetCadLroc`. Analyzing this data requires methods described in the book, implemented in the function `StSignificanceTestingCadVsRad`.

Usage

```
dataset09
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1, 1:10, 1:200, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1, 1:10, 1:80, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:80], number of lesions per diseased case
- `lesions$IDs`, num [1:80, 1], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:80, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset09", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "NICO-CAD-ROC", the name of the dataset
- `descriptions$truthTableStr`, num [1, 1:10, 1:200, 1:2], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr "1", treatment label(s)
- `descriptions$readerID`, chr [1:10] "1" "2" "3" "4" ..., reader labels

References

Hupse R et al. Standalone computer-aided detection compared to radiologists' performance for the detection of mammographic masses. Eur Radiol. 2013;23(1):93-100.

Examples

```
str(dataset09)
PlotEmpiricalOperatingCharacteristics(dataset = dataset09, rdrs = 1:10, opChType = "ROC")$Plot
```

`dataset10` *Marc Ruschin ROC dataset*

Description

This is referred to in the book as the "RUS" dataset. It consists of 90 cases, 40 of which are diseased, the images were acquired at three dose levels, which can be regarded as treatments. "0" = conventional film radiographs, "1" = digitized images viewed on monitors, Eight radiologists interpreted the cases using the FROC paradigm. These have been reduced to ROC data by using the highest ratings (the original FROC data is lost).

Usage

```
dataset10
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:3, 1:8, 1:90, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:3, 1:8, 1:40, 1] , ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:40], number of lesions per diseased case
- `lesions$IDs`, num [1:40, 1], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:40, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset10", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "RUSCHIN", the name of the dataset
- `descriptions$truthTableStr`, num [1:3, 1:8, 1:90, 1:2], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:3] "1" "2" "3", treatment label(s)
- `descriptions$readerID`, chr [1:8] "1" "2" "3" "4" ..., reader labels

References

Ruschin M, et al. Dose dependence of mass and microcalcification detection in digital mammography: free response human observer studies. Med Phys. 2007;34:400 - 407.

Examples

```
str(dataset10)
PlotEmpiricalOperatingCharacteristics(dataset = dataset10, opChType = "ROC")$Plot
```

dataset11 *Dobbins 1 FROC dataset*

Description

This is referred to in the book as the "DOB1" dataset. Dobbins et al conducted a multi-institutional, MRMC study to compare the performance of digital tomosynthesis (GE's VolumeRad device), dual-energy (DE) imaging, and conventional chest radiography for pulmonary nodule detection and management. All study images were obtained with a flat-panel detector developed by GE. The case set consisted of 158 subjects, of which 43 were non-diseased and the rest had 1 - 20 pulmonary nodules independently verified, using with CT images, by 3 experts who did not participate in the observer study. The study used FROC paradigm data collection. There are 4 treatments labeled 1 - 4 (conventional chest x-ray, CXR, CXR augmented with dual-energy (CXR+DE), VolumeRad digital tomosynthesis images and VolumeRad augmented with DE (VolumeRad+DE).

Usage

```
dataset11
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:4, 1:5, 1:158, 1:4], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:4, 1:5, 1:115, 1:20], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:115], number of lesions per diseased case
- `lesions$IDs`, num [1:115, 1:20], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:115, 1:20], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset11", base name of dataset in 'data' folder
- `descriptions$type`, chr "FROC", the data type
- `descriptions$name`, chr "DOBBINS-1", the name of the dataset
- `descriptions$truthTableStr`, num [1:4, 1:5, 1:158, 1:21], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:4] "1" "2" "3" "4", treatment label(s)
- `descriptions$readerID`, chr [1:5] "1" "2" "3" "4" ..., reader labels

References

Dobbins III JT et al. Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 2016;282(1):236-250.

Examples

```
str(dataset11)
```

`dataset12` *Dobbins 2 ROC dataset*

Description

This is referred to in the code as the "DOB2" dataset. It contains actionability ratings, i.e., do you recommend further follow up on the patient, one a 1 (definitely not) to 5 (definitely yes), effectively an ROC dataset using a 5-point rating scale.

Usage

```
dataset12
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:4, 1:5, 1:152, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:4, 1:5, 1:88, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:88], number of lesions per diseased case
- `lesions$IDs`, num [1:88, 1], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:88, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset12", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "DOBBINS-2", the name of the dataset
- `descriptions$truthTableStr`, num [1:4, 1:5, 1:152, 1:2] , truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:4] "1" "2" "3" "4", treatment label(s)
- `descriptions$readerID`, chr [1:5] "1" "2" "3" "4" ..., reader labels

References

Dobbins III JT et al. Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 2016;282(1):236-250.

Examples

```
str(dataset12)
```

`dataset13` *Dobbins 3 FROC dataset*

Description

This is referred to in the code as the "DOB3" dataset. This is a subset of DOB1 which includes data for lesions not-visible on CXR, but visible to truth panel on all treatments.

Usage

```
dataset13
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:4, 1:5, 1:158, 1:4], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:4, 1:5, 1:106, 1:15], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:106], number of lesions per diseased case
- `lesions$IDs`, num [1:106, 1:15], numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:106, 1:15], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset13", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "FROC", the data type
- `descriptions$name`, chr "DOBBINS-3", the name of the dataset
- `descriptions$truthTableStr`, num [1:4, 1:5, 1:158, 1:16], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:4] "1" "2" "3" "4", treatment label(s)
- `descriptions$readerID`, chr [1:5] "1" "2" "3" "4" ..., reader labels

References

Dobbins III JT et al. Multi-Institutional Evaluation of Digital Tomosynthesis, Dual-Energy Radiography, and Conventional Chest Radiography for the Detection and Management of Pulmonary Nodules. Radiology. 2016;282(1):236-250.

Examples

```
str(dataset13)
```

`dataset14` *Federica Zanca real (as opposed to inferred) ROC dataset*

Description

This is referred to in the book as the "FZR" dataset. It is a real ROC study, conducted on the same images and using the same radiologists, on treatments "4" and "5" of dataset04. This was compared to highest rating inferred ROC data from dataset04 to conclude, erroneously, that the highest rating assumption is invalid. See book Section 13.6.2.

Usage

```
dataset14
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:2, 1:4, 1:200, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:2, 1:4, 1:100, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:100], number of lesions per diseased case
- `lesions$IDs`, num [1:100, 1] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:100, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "dataset14", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "FEDERICA-REAL-ROC", the name of the dataset
- `descriptions$truthTableStr`, num [1:2, 1:4, 1:200, 1:2], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr [1:2] "4" "5", treatment label(s)
- `descriptions$readerID`, chr [1:4] "1" "2" "3" "4", reader labels

References

Zanca F, Hillis SL, Claus F, et al (2012) Correlation of free-response and receiver-operating-characteristic area-under-the-curve estimates: Results from independently conducted FROC/ROC studies in mammography. Med Phys. 39(10):5917-5929.

Examples

```
str(dataset14)
```

---

datasetBinned123 *Binned dataset suitable for checking* FitCorCbm*; seed = 123*

Description

A binned dataset suitable for analysis by FitCorCbm. It was generated by DfCreateCorCbmDataset by setting the seed variable to 123. Note the formatting of the data as a single treatment two reader dataset, even though the actual pairing might be different, see FitCorCbm. The dataset is intentionally large so as to demonstrate the asymptotic convergence of ML estimates, produced by FitCorCbm, to the population values. The data was generated by the following argument values to DfCreateCorCbmDataset: seed = 123, K1 = 5000, K2 = 5000, desiredNumBins = 5, muX = 1.5, muY = 3, alphaX = 0.4, alphaY = 0.7, rhoNor = 0.3, rhoAbn2 = 0.8.

Usage

```
datasetBinned123
```

Format

A list with 3 elements: $ratings, $lesions and $descriptions; $ratings contain 3 elements, $NL, $LL and $LL_IL as sub-lists; $lesions contain 3 elements, $perCase, $IDs and $weights as sub-lists; $descriptions contain 7 elements, $fileName, $type, $name, $truthTableStr, $design, $modalityID and $readerID as sub-lists;

- rating$NL, num [1, 1:2, 1:10000, 1], ratings of non-lesion localizations, NLs
- rating$LL, num [1, 1:2, 1:5000, 1], ratings of lesion localizations, LLs
- rating$LL_ILNA, this placeholder is used only for LROC data
- lesions$perCase, int [1:5000], number of lesions per diseased case
- lesions$IDs, num [1:5000, 1] , numeric labels of lesions on diseased cases
- lesions$weights, num [1:5000, 1], weights (or clinical importances) of lesions
- descriptions$fileName, chr, "datasetBinned123", base name of dataset in ‘data‘ folder
- descriptions$type, chr "ROC", the data type
- descriptions$name, chr "SIM-CORCBM-SEED-123", the name of the dataset
- descriptions$truthTableStr, NA, truth table structure
- descriptions$design, chr "FCTRL-X-MOD", study design, factorial dataset
- descriptions$modalityID, chr "1", treatment label(s)
- descriptions$readerID, chr [1:2] "1" "2", reader labels

References

Zhai X, Chakraborty DP (2017). A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
str(datasetBinned123)
```

`datasetBinned124` *Binned dataset suitable for checking* `FitCorCbm`*; seed = 124*

Description

A binned dataset suitable for analysis by `FitCorCbm`. It was generated by `DfCreateCorCbmDataset` by setting the `seed` variable to 124. Otherwise similar to `datasetBinned123`.

Usage

```
datasetBinned124
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1, 1:2, 1:10000, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1, 1:2, 1:5000, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:5000], number of lesions per diseased case
- `lesions$IDs`, num [1:5000, 1] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:5000, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetBinned124", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "SIM-CORCBM-SEED-124", the name of the dataset
- `descriptions$truthTableStr`, NA, truth table structure
- `descriptions$design`, chr "FCTRL-X-MOD", study design, factorial dataset
- `descriptions$modalityID`, chr "1", treatment label(s)
- `descriptions$readerID`, chr [1:2] "1" "2", reader labels

References

Zhai X, Chakraborty DP (2017). A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
str(datasetBinned124)
```

`datasetBinned125` *Binned dataset suitable for checking* `FitCorCbm`*; seed = 125*

Description

A binned dataset suitable for analysis by `FitCorCbm`. It was generated by `DfCreateCorCbmDataset` by setting the `seed` variable to 125. Otherwise similar to `datasetBinned123`.

Usage

```
datasetBinned125
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1, 1:2, 1:10000, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1, 1:2, 1:5000, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:5000], number of lesions per diseased case
- `lesions$IDs`, num [1:5000, 1] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:5000, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetBinned125", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "SIM-CORCBM-SEED-125", the name of the dataset
- `descriptions$truthTableStr`, NA, truth table structure
- `descriptions$design`, chr "FCTRL-X-MOD", study design, factorial dataset
- `descriptions$modalityID`, chr "1", treatment label(s)
- `descriptions$readerID`, chr [1:2] "1" "2", reader labels

References

Zhai X, Chakraborty DP (2017). A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
str(datasetBinned125)
```

`datasetCadLroc` *Nico Karssemeijer LROC dataset (CAD vs. radiologists)*

Description

This is the actual LROC data corresponding to `dataset09`, which was the inferred ROC data. Note that the `LL` field is split into two, `LL`, representing true positives where the lesions were correctly localized, and `LL_IL`, representing true positives where the lesions were incorrectly localized. The first reader is CAD and the remaining readers are radiologists.

Usage

```
datasetCadLroc
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1, 1:10, 1:200, 1], ratings of localizations on normal cases
- `rating$LL`, num [1, 1:10, 1:80, 1], ratings of correct localizations on abnormal cases
- `rating$LL_ILnum` [1, 1:10, 1:80, 1], ratings of incorrect localizations on abnormal cases
- `lesions$perCase`, int [1:80], number of lesions per diseased case
- `lesions$IDs`, num [1:80, 1] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:80, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetCadLroc", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "LROC", the data type
- `descriptions$name`, chr "NICO-CAD-LROC", the name of the dataset
- `descriptions$truthTableStr`, num [1:2, 1:4, 1:200, 1:2], truth table structure
- `descriptions$design`, chr "FCTRL", study design, factorial dataset
- `descriptions$modalityID`, chr "1", treatment label(s)
- `descriptions$readerID`, chr [1:10] "1" "2" "3" "4" ..., reader labels

References

Hupse R et al. Standalone computer-aided detection compared to radiologists' performance for the detection of mammographic masses. Eur Radiol. 2013;23(1):93-100.

Examples

```
str(datasetCadLroc)
```

`datasetCadSimuFroc` *Simulated FROC CAD vs. RAD dataset*

Description

Simulated FROC CAD vs. RAD dataset suitable for checking code. It was generated from datasetCadLroc using SimulateFrocFromLrocData.R. The LROC paradigm always yields a single mark per case. Therefore the equivalent FROC will also have only one mark per case. The NL arrays of the two datasets are identical. The LL array is created by copying the LL (correct localiztion) array of the LROC dataset to the LL array of the FROC dataset, from diseased case index k2 = 1 to k2 = K2. Additionally, the LL_IL array of the LROC dataset is copied to the NL array of the FROC dataset, starting at case index k1 = K1+1 to k1 = K1+K2. Any zero ratings are replace by -Infs. The equivalent FROC dataset has the same HrAuc as the original LROC dataset. See example. The main use of this dataset & function is to test the CAD significance testing functions using CAD FROC datasets, which I currently don't have.

Usage

```
datasetCadSimuFroc
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1, 1:10, 1:200, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1, 1:10, 1:80, 1], ratings of lesion localizations, LLs
- `rating$LL_ILNA`, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:80], number of lesions per diseased case
- `lesions$IDs`, num [1:80, 1] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:80, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetCadSimuFroc", base name of dataset in 'data' folder
- `descriptions$type`, chr "LROC", the data type

- descriptions$name, chr "NICO-CAD-LROC", the name of the dataset
- descriptions$truthTableStr, num [1:2, 1:4, 1:200, 1:2], truth table structure
- descriptions$design, chr "FCTRL", study design, factorial dataset
- descriptions$modalityID, chr "1", treatment label(s)
- descriptions$readerID, chr [1:10] "1" "2" "3" "4" ..., reader labels

---

datasetCrossedModality

John Thompson crossed treatment FROC dataset

Description

This is a crossed treatment dataset, see book Section 18.5. There are two treatment factors. The first treatment factor modalityID1 can be "F" or "I", which represent two CT reconstruction algorithms. The second treatment factor modalityID2 can be "20" "40" "60" "80", which represent the mAs values of the image acquisition. The factors are fully crossed. The function StSignificanceTestingCrossedModalities analyzes such datasets.

Usage

```
datasetCrossedModality
```

Format

A list with 3 elements: $ratings, $lesions and $descriptions; $ratings contain 3 elements, $NL, $LL and $LL_IL as sub-lists; $lesions contain 3 elements, $perCase, $IDs and $weights as sub-lists; $descriptions contain 7 elements, $fileName, $type, $name, $truthTableStr, $design, $modalityID and $readerID as sub-lists;

- rating$NL, num [1:2, 1:4, 1:11, 1:68, 1:5], ratings of non-lesion localizations, NLs
- rating$LL, num [1:2, 1:4, 1:11, 1:34, 1:3], ratings of lesion localizations, LLs
- rating$LL_ILNA, this placeholder is used only for LROC data
- lesions$perCase, int [1:34], number of lesions per diseased case
- lesions$IDs, num [1:34, 1:3] , numeric labels of lesions on diseased cases
- lesions$weights, num [1:34, 1:3], weights (or clinical importances) of lesions
- descriptions$fileName, chr, "datasetCrossedModality", base name of dataset in ‘data‘ folder
- descriptions$type, chr "FROC", the data type
- descriptions$name, chr "THOMPSON-X-MOD", the name of the dataset
- descriptions$truthTableStr, NA, truth table structure
- descriptions$design, chr "FCTRL-X-MOD", study design, factorial dataset
- descriptions$modalityID, chr [1:2] "F" "I", treatment label(s)
- descriptions$readerID, chr [1:4] "20" "40" "60" "80", reader labels

References

Thompson JD, Chakraborty DP, Szczepura K, et al. (2016) Effect of reconstruction methods and x-ray tube current-time product on nodule detection in an anthropomorphic thorax phantom: a crossed-treatment JAFROC observer study. Medical Physics. 43(3):1265-1274.

Examples

```
str(datasetCrossedModality)
```

`datasetDegenerate` *Simulated degenerate ROC dataset (for testing purposes)*

Description

A simulated degenerated dataset. A degenerate dataset is defined as one with no interior operating points on the ROC plot. Such data tend to be observed with expert level radiologists. This dataset is used to illustrate the robustness of two fitting models, namely CBM and RSM. The widely used binormal model and PROPROC fail on such datasets.

Usage

```
datasetDegenerate
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1, 1, 1:15, 1], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1, 1, 1:10, 1], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:10], number of lesions per diseased case
- `lesions$IDs`, num [1:10, 1] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:10, 1], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetDegenerate", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROC", the data type
- `descriptions$name`, chr "SIM-DEGENERATE", the name of the dataset
- `descriptions$truthTableStr`, NA, truth table structure
- `descriptions$design`, chr "FCTRL-X-MOD", study design, factorial dataset
- `descriptions$modalityID`, chr "1", treatment label(s)
- `descriptions$readerID`, chr "1", reader labels

Examples

```
str(datasetDegenerate)
```

`datasetFROCSpC` *Simulated FROC SPLIT-PLOT-C dataset*

Description

Simulated from FED Excel dataset by successively ignoring readers 3:4, c(1,3:4), c(1:2,4), etc. created simulated split plot Excel dataset from Fed dataset: confirmed it is read without error

Usage

```
datasetFROCSpC
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:2, 1:4, 1:200, 1:7], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:2, 1:4, 1:100, 1:3], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:100], number of lesions per diseased case
- `lesions$IDs`, num [1:100, 1:3] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:100, 1:3], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetFROCSpC", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "FROC", the data type
- `descriptions$name`, chr "SIM-FROC-SPLIT-PLOT-C", the name of the dataset
- `descriptions$truthTableStr`, NA, truth table structure
- `descriptions$design`, chr "FCTRL-X-MOD", study design, factorial dataset
- `descriptions$modalityID`, chr [1:2] "4" "5", treatment label(s)
- `descriptions$readerID`, chr [1:4] "1" "3" "4" "5", reader labels

Examples

```
str(datasetFROCSpC)
```

datasetROI *Simulated ROI dataset*

Description

TBA Simulated ROI dataset: assumed are 4 ROIs per case, 5 readers, 50 non-dieased and 40 diseased cases.

Usage

```
datasetROI
```

Format

A list with 3 elements: `$ratings`, `$lesions` and `$descriptions`; `$ratings` contain 3 elements, `$NL`, `$LL` and `$LL_IL` as sub-lists; `$lesions` contain 3 elements, `$perCase`, `$IDs` and `$weights` as sub-lists; `$descriptions` contain 7 elements, `$fileName`, `$type`, `$name`, `$truthTableStr`, `$design`, `$modalityID` and `$readerID` as sub-lists;

- `rating$NL`, num [1:2, 1:5, 1:90, 1:4], ratings of non-lesion localizations, NLs
- `rating$LL`, num [1:2, 1:5, 1:40, 1:4], ratings of lesion localizations, LLs
- `rating$LL_IL`NA, this placeholder is used only for LROC data
- `lesions$perCase`, int [1:40], number of lesions per diseased case
- `lesions$IDs`, num [1:40, 1:4] , numeric labels of lesions on diseased cases
- `lesions$weights`, num [1:40, 1:4], weights (or clinical importances) of lesions
- `descriptions$fileName`, chr, "datasetROI", base name of dataset in ‘data‘ folder
- `descriptions$type`, chr "ROI", the data type
- `descriptions$name`, chr "SIM-ROI", the name of the dataset
- `descriptions$truthTableStr`, NA, truth table structure
- `descriptions$design`, chr "FCTRL-X-MOD", study design, factorial dataset
- `descriptions$modalityID`, chr [1:2] "1" "2", treatment label(s)
- `descriptions$readerID`, chr [1:5] "1" "2" "3" "4" ..., reader labels

Examples

```
str(datasetROI)
```

`Df2RJafrocDataset` *Convert ratings arrays to an RJafroc dataset*

Description

Converts ratings arrays, ROC or FROC, *but not LROC*, to an **RJafroc** dataset, thereby allowing the user to leverage the file I/O, plotting and analyses capabilities of **RJafroc**.

Usage

```
Df2RJafrocDataset(NL, LL, InputIsCountsTable = FALSE, ...)
```

Arguments

`NL`	Non-lesion localizations array (or FP array for ROC data).
`LL`	Lesion localizations array (or TP array for ROC data).
`InputIsCountsTable`	If `TRUE`, the `NL` and `LL` arrays are rating-counts tables, with common lengths equal to the number of ratings `R`, if `FALSE`, the default, these are arrays of lengths `K1`, the number of non-diseased cases, and `K2`, the number of diseased cases, respectively.
`...`	Other elements of **RJafroc** dataset that may, depending on the context, need to be specified. `perCase` **must** be specified if an FROC dataset is to be returned. It is a `K2`-length array specifying the numbers of lesions in each diseased case in the dataset.

Details

The function "senses" the data type (ROC or FROC) from the the absence or presence of `perCase`.

- ROC data can be `NL[1:K1]` and `LL[1:K2]` or `NL[1:I,1:J,1:K1]` and `LL[1:I,1:J,1:K2]`.
- FROC data can be `NL[1:K1,1:maxNL]` and `LL[1:K2,1:maxLL]` or `NL[1:I,1:J,1:K1,1:maxNL]` and `LL[1:I,1:J,1:K2,1:maxLL]`.

Here `maxNL`/`maxLL` = maximum numbers of NLs/LLs, per case, over entire dataset. Equal weights are assigned to every lesion (FROC data). Consecutive characters/integers starting with "1" are assigned to `IDs`, `modalityID` and `readerID`.

Value

A dataset with the structure described in `RJafroc-package`.

Examples

```
## Input as ratings arrays
set.seed(1);NL <- rnorm(5);LL <- rnorm(7)*1.5 + 2
dataset <- Df2RJafrocDataset(NL, LL)

## Input as counts tables
K1t <- c(30, 19, 8, 2, 1)
K2t <- c(5,  6, 5, 12, 22)
dataset <- Df2RJafrocDataset(K1t, K2t, InputIsCountsTable = TRUE)
```

`DfBinDataset` *Returns a binned dataset*

Description

Bins continuous (i.e. floating point) or quasi-continuous (e.g. integers 0-100) ratings in a dataset and returns the corresponding binned dataset in which the ratings are integers 1, 2,...., with higher values representing greater confidence in presence of disease

Usage

```
DfBinDataset(dataset, desiredNumBins = 7, opChType)
```

Arguments

`dataset`	The dataset to be binned, with structure as in `RJafroc-package`.
`desiredNumBins`	The desired number of bins. The default is 7.
`opChType`	The operating characteristic relevant to the binning operation: `"ROC"`, `"FROC"`, `"AFROC"`, or `"wAFROC"`.

Details

For small datasets the number of bins may be smaller than `desiredNumBins`. **The algorithm needs to know the type of operating characteristic relevant to the binning operation.** For ROC the bins are FP and TP counts, for FROC the bins are NL and LL counts, for AFROC the bins are FP and LL counts, and for wAFROC the bins are FP and wLL counts. Binning is generally employed prior to fitting a statistical model, e.g., maximum likelihood, to the data. This version chooses ctffs so as to maximize empirical AUC (this yields a unique choice of ctffs which gives the reader the maximum deserved credit).

Value

The binned dataset

References

Miller GA (1956) The Magical Number Seven, Plus or Minus Two: Some limits on our capacity for processing information, The Psychological Review 63, 81-97

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
binned <- DfBinDataset(dataset02, desiredNumBins = 3, opChType = "ROC")
binned <- DfBinDataset(dataset05, desiredNumBins = 4, opChType = "ROC")
binned <- DfBinDataset(dataset05, desiredNumBins = 4, opChType = "AFROC")
binned <- DfBinDataset(dataset05, desiredNumBins = 4, opChType = "wAFROC")
binned <- DfBinDataset(dataset05, opChType = "wAFROC", desiredNumBins = 1)
binned <- DfBinDataset(dataset05, opChType = "wAFROC", desiredNumBins = 2)
binned <- DfBinDataset(dataset05, opChType = "wAFROC", desiredNumBins = 3)
## etc.



## takes longer than 5 sec on OSX
dataset <- SimulateRocDataset(I = 2, J = 5, K1 = 50, K2 = 70, a = 1, b = 0.5, seed = 123)
datasetB <- DfBinDataset(dataset, desiredNumBins = 7, opChType = "ROC")
fomOrg <- as.matrix(UtilFigureOfMerit(dataset, FOM = "Wilcoxon"))
print(fomOrg)
fomBinned <- as.matrix(UtilFigureOfMerit(datasetB, FOM = "Wilcoxon"))
print(fomBinned)
cat("mean, sd = ", mean(fomOrg), sd(fomOrg), "\n")
cat("mean, sd = ", mean(fomBinned), sd(fomBinned), "\n")
```

DfCreateCorCbmDataset *Create paired dataset for testing* FitCorCbm

---

Description

The paired dataset is generated using bivariate sampling; details are in referenced publication

Usage

```
DfCreateCorCbmDataset(
  seed = 123,
  K1 = 50,
  K2 = 50,
  desiredNumBins = 5,
  muX = 1.5,
```

```
  muY = 3,
  alphaX = 0.4,
  alphaY = 0.7,
  rhoNor = 0.3,
  rhoAbn2 = 0.8
)
```

Arguments

seed	The seed variable, default is 123; set to NULL for truly random seed
K1	The number of non-diseased cases, default is 50
K2	The number of diseased cases, default is 50
desiredNumBins	The desired number of bins; default is 5
muX	The CBM μ parameter in condition X
muY	The CBM μ parameter in condition Y
alphaX	The CBM α parameter in condition X
alphaY	The CBM 'alpha' parameter in condition Y
rhoNor	The correlation of non-diseased case z-samples
rhoAbn2	The correlation of diseased case z-samples, when disease is visible in both conditions

Details

The ROC data is bined to 5 bins in each condition.

Value

The return value is the desired dataset, suitable for testing FitCorCbm.

References

Zhai X, Chakraborty DP (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
## seed <- 1
## this gives unequal numbers of bins in X and Y conditions for 50/50 dataset
dataset <- DfCreateCorCbmDataset()


## this takes very long time!! used to show asymptotic convergence of ML estimates
## dataset <- DfCreateCorCbmDataset(K1 = 5000, K2 = 5000)
```

DfExtractCorCbmDataset *Extract two arms of a pairing from an MRMC ROC dataset*

Description

Extract a paired dataset from a larger dataset. The pairing could be two readers in the same treatment, or different readers in different treatments, or the same reader in different treatments. If necessary The data is binned to 5 bins in each condition.

Usage

```
DfExtractCorCbmDataset(dataset, trts = 1, rdrs = 1)
```

Arguments

dataset	The original dataset from which the pairing is to be extracted
trts	A vector, maximum length 2, contains the indices of the treatment or treatments to be extracted
rdrs	A vector, maximum length 2, contains the indices of the reader or readers to be extracted

Details

The desired pairing is contained in the vectors `trts` and `rdrs`. If either has length one, the other must have length two and the pairing is implicit. If both are length two, then the pairing is that implied by the first treatement and the second reader, which is one arm, and the other arm is that implied by the second treatment paired with the first reader. Using this method any allowed pairing can be extracted and analyzed by `FitCorCbm`. The utility of this software is in designing a ratings simulator that is statistically matched to a real dataset.

Value

A new dataset in which the number of treatments is one and the number of readers is two

Examples

```
## Extract the paired data corresponding to the second and third readers in the first treatment
## from the included ROC dataset
dataset11_23 <- DfExtractCorCbmDataset(dataset05, trts = 1, rdrs = c(2,3))

## Extract the paired data corresponding to the third reader in the first and second treatments
dataset12_33 <- DfExtractCorCbmDataset(dataset05, trts = c(1,2), rdrs = 3)

## Extract the data corresponding to the first reader in the first
## treatment paired with the data
```

```
## from the third reader in the second treatment
## (the bin indices are at different positions in the two arrays)
dataset12_13 <- DfExtractCorCbmDataset(dataset05,
trts = c(1,2), rdrs = c(1,3))
```

`DfExtractDataset` *Extract a subset of treatments and readers from a dataset*

Description

Extract a dataset consisting of a subset of treatments/readers from a larger dataset

Usage

```
DfExtractDataset(dataset, trts, rdrs)
```

Arguments

`dataset`	The original dataset from which the subset is to be extracted
`trts`	A vector contains the indices of the treatments to be extracted. **If this parameter is not supplied, all treatments are extracted.**
`rdrs`	A vector contains the indices of the readers to be extracted. **If this parameter is not supplied, all readers are extracted.**

Details

Note that `trts` and `rdrs` are the vectors of **indices** not **IDs**. For example, if the ID of the first reader is "0", the corresponding value in `trts` should be **1** not **0**.

Value

A new dataset containing only the specified treatments and readers that were extracted from the original dataset

Examples

```
## Extract the data corresponding to the second reader in the
## first treatment from an included ROC dataset
ds1 <- DfExtractDataset(dataset05, trts = 1, rdrs = 2)

## Extract the data of the first and third reader in all
## treatment from the included ROC dataset
ds2 <- DfExtractDataset(dataset05, rdrs = c(1, 3))
```

`DfFroc2Lroc` *Simulates an "AUC-equivalent" LROC dataset from an FROC dataset*

Description

Simulates a multiple-treatment multiple-reader "AUC-equivalent" LROC dataset from a supplied FROC dataset.

Usage

```
DfFroc2Lroc(dataset)
```

Arguments

`dataset`	The FROC dataset to be converted to LROC.

Details

The FROC paradigm can have 0 or more marks per case. However, LROC is restricted to **exactly one mark per case**. For the NL array of the LROC data, for non-disesed cases, the **highest** rating of the FROC marks, or -Inf if there are no marks, is copied to case index k1 = 1 to k1 = K1 of the LROC dataset. For each diseased case, if the max LL rating exceeds the max NL rating, then the max LL rating is copied to the LL array, otherwise the max NL rating is copied to the LL_IL array. The max NL rating on each diseased case is then set to -Inf (since the LROC paradigm only allows one mark. The equivalent FROC dataset has the same HrAuc as the original LROC dataset. See example. The main use of this function is to test the Significance testing functions using MRMC LROC datasets, which I currently don't have.

Value

The equivalent LROC dataset

Examples

```
lrocDataset <- DfFroc2Lroc(dataset05)
frocHrAuc <- UtilFigureOfMerit(dataset05, FOM = "HrAuc")
lrocWilcoxonAuc <- UtilFigureOfMerit(lrocDataset, FOM = "Wilcoxon")
## expect_equal(frocHrAuc, lrocWilcoxonAuc)
```

DfFroc2Roc *Convert an FROC dataset to an ROC dataset*

Description

Convert an FROC dataset to a highest rating inferred ROC dataset

Usage

```
DfFroc2Roc(dataset)
```

Arguments

dataset	The FROC dataset to be converted, RJafroc-package.

Details

The first member of the ROC dataset is NL, whose 3rd dimension has length (K1 + K2), the total number of cases. Ratings of cases (K1 + 1) through (K1 + K2) are -Inf. **This is because in an ROC dataset FPs are only possible on non-diseased cases.**The second member of the list is LL. Its 3rd dimension has length K2, the number of diseased cases. **This is because TPs are only possible on diseased cases**. For each case the inferred ROC rating is the highest of all FROC ratings on that case. If a case has no marks, a **finite ROC rating, guaranteed to be smaller than the rating on any marked case**, is assigned to it. The dataset structure is shown below:

- NL Ratings array [1:I, 1:J, 1:(K1+K2), 1], of false positives, FPs
- LL Ratings array [1:I, 1:J, 1:K2, 1], of true positives, TPs
- perCase array [1:K2], number of lesions per diseased case
- IDs array [1:K2, 1], labels of lesions on diseased cases
- weights array [1:K2, 1], weights (or clinical importances) of lesions
- dataType "ROC", the data type
- modalityID [1:I] inherited modality labels
- readerID [1:J] inherited reader labels

Value

An ROC dataset with **finite ratings** in NL[,,1:K1,1] and LL[,,1:K2,1].

Examples

```
rocDataSet <- DfFroc2Roc(dataset05)
rocSpDataSet <- DfFroc2Roc(datasetFROCSpC)

## in the following example, because of the smaller number of cases,
## it is easy to see the process at work:
```

```
set.seed(1);K1 <- 3;K2 <- 5
mu <- 1;nuP <- 0.5;lambdaP <- 2;zeta1 <- 0
lambda <- UtilPhysical2IntrinsicRSM(mu,lambdaP,nuP)$lambda
nu <- UtilPhysical2IntrinsicRSM(mu,lambdaP,nuP)$nu
Lmax <- 2;Lk2 <- floor(runif(K2, 1, Lmax + 1))
frocDataRaw <- SimulateFrocDataset(mu, lambda, nu, zeta1, I = 1, J = 1,
K1, K2, perCase = Lk2)
hrData <- DfFroc2Roc(frocDataRaw)

## print("frocDataRaw$ratings$NL[1,1,,] = ")
## print("hrData$ratings$NL[1,1,1:K1,] = ")
## print("frocDataRaw$ratings$LL[1,1,,] = ")
## print("hrData$ratings$LL[1,1,,] = ")

## following is the output

## [1] "frocDataRaw$ratings$NL[1,1,,] = "
## [,1]      [,2]      [,3] [,4]
## [1,] 2.4046534 0.7635935      -Inf -Inf
## [2,]      -Inf      -Inf      -Inf -Inf
## [3,] 0.2522234      -Inf      -Inf -Inf
## [4,] 0.4356833      -Inf      -Inf -Inf
## [5,]      -Inf      -Inf      -Inf -Inf
## [6,]      -Inf      -Inf      -Inf -Inf
## [7,]      -Inf      -Inf      -Inf -Inf
## [8,] 0.8041895 0.3773956 0.1333364 -Inf

## > ## print("hrData$ratings$NL[1,1,1:K1,] = ")
## [1] "hrData$ratings$NL[1,1,1:K1,] = "
## [1] 2.4046534      -Inf 0.2522234
## > ## print("frocDataRaw$ratings$LL[1,1,,] = ")
## [1] "frocDataRaw$ratings$LL[1,1,,] = "
## [,1] [,2]
## [1,]      -Inf -Inf
## [2,] 1.5036080 -Inf
## [3,] 0.8442045 -Inf
## [4,] 1.0467262 -Inf
## [5,]      -Inf -Inf
## > ## print("hrData$ratings$LL[1,1,,] = ")
## [1] "hrData$ratings$LL[1,1,,] = "
## [1] 0.4356833 1.5036080 0.8442045 1.0467262 0.8041895
## Note that rating of the first and the last diseased case came from NL marks
```

DfLroc2Froc *Simulates an "AUC-equivalent" FROC dataset from an LROC dataset*

Description

Simulates a multiple-treatment multiple-reader "AUC-equivalent" FROC dataset from a supplied LROC dataset, e.g., datasetCadLroc.

Usage

```
DfLroc2Froc(dataset)
```

Arguments

dataset	The LROC dataset to be converted to FROC.

Details

The LROC paradigm always yields a single mark per case. Therefore the equivalent FROC will also have only one mark per case. The NL arrays of the two datasets are identical. The LL array is created by copying the LLCl array of the LROC dataset to the LL array of the FROC dataset, from diseased case index k2 = 1 to k2 = K2. Additionally, the LLIl array of the LROC dataset is copied to the NL array of the FROC dataset, starting at case index k1 = K1+1 to k1 = K1+K2. Any zero ratings are replace by -Infs. The equivalent FROC dataset has the same HrAuc as the original LROC dataset. See example. The main use of this function is to test the CAD significance testing functions using CAD FROC datasets, which I currently don't have.

Value

The equivalent FROC dataset

Examples

```
frocDataset <- DfLroc2Froc(datasetCadLroc)
lrocAuc <- UtilFigureOfMerit(datasetCadLroc, FOM = "Wilcoxon")
frocHrAuc <- UtilFigureOfMerit(frocDataset, FOM = "HrAuc")
```

DfLroc2Roc *Convert an LROC dataset to a ROC dataset*

Description

Converts an LROC dataset to an ROC dataset

Usage

```
DfLroc2Roc(dataset)
```

Arguments

dataset	The **LROC** dataset to be converted.

Details

For the diseased cases one takes the maximum rating on each diseased case, which could be a LL ("true positive" correct localization) or a LL_IL ("true positive" incorrect localization) rating, whichever has the higher rating. For non-diseased cases the NL arrays are identical.

Value

An ROC dataset

Examples

```
rocDataSet <- DfLroc2Roc(datasetCadLroc)
```

`DfReadCrossedModalities` *Read a crossed-treatment data file*

Description

Read an crossed-treatment data file, in which the two treatment factors are crossed

Usage

```
DfReadCrossedModalities(fileName, sequentialNames = FALSE)
```

Arguments

`fileName`	A string specifying the name of the file that contains the dataset, which must be an extended-JAFROC format data file containing an additional treatment factor.
`sequentialNames`	If `TRUE`, consecutive integers (starting from 1) will be used as the treatment and reader IDs. Otherwise, treatment and reader IDs in the original data file will be used. The default is `FALSE`.

Details

The data format is similar to the JAFROC format (see `RJafroc-package`). The notable difference is that there are two treatment factors.

Value

A dataset with the specified structure, similar to a standard **RJafroc** dataset (see `RJafroc-package`). Because of the extra treatment factor, `NL` and `LL` are each five dimensional arrays. There are also two treatment IDS: `modalityID1` and `modalityID2`.

References

Thompson JD, Chakraborty DP, Szczepura K, et al. (2016) Effect of reconstruction methods and x-ray tube current-time product on nodule detection in an anthropomorphic thorax phantom: a crossed-treatment JAFROC observer study. Medical Physics. 43(3):1265-1274.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

`DfReadDataFile` *Read a data file*

Description

Read a disk file and create a dataset object from it.

Usage

```
DfReadDataFile(
  fileName,
  format = "JAFROC",
  newExcelFileFormat = FALSE,
  delimiter = ",",
  sequentialNames = FALSE
)
```

Arguments

`fileName`	A string specifying the name of the file. The file-extension must match the format specified below
`format`	A string specifying the format of the data in the file. It can be `"JAFROC"`, the default, which requires a .xlsx Excel file, **not .xls**, `"MRMC"` or `"iMRMC"`.
`newExcelFileFormat`	This argument only applies to the `"JAFROC"` format. The default is `FALSE`. if `TRUE` the function accommodates 3 additional columns in the `Truth` worksheet. If `FALSE`, the original function (as in version 1.2.0) is used and the three extra columns, if present, throws an error.
`delimiter`	The string delimiter to be used for the `"MRMC"` format (`","` is the default). This parameter is not used when reading `"JAFROC"` or `"iMRMC"` data files.
`sequentialNames`	A logical variable: if `TRUE`, consecutive integers (starting from 1) will be used as the treatment and reader IDs (i.e., names). Otherwise, treatment and reader IDs in the original data file will be used.

Value

A dataset with the structure specified in `RJafroc-package`.

Examples

```
fileName <- system.file("extdata", "Roc.xlsx",
package = "RJafroc", mustWork = TRUE)
RocDataXlsx <- DfReadDataFile(fileName)

fileName <- system.file("extdata", "RocData.csv",
package = "RJafroc", mustWork = TRUE)
RocDataCsv<- DfReadDataFile(fileName, format = "MRMC")

fileName <- system.file("extdata", "RocData.imrmc",
package = "RJafroc", mustWork = TRUE)
RocDataImrmc<- DfReadDataFile(fileName, format = "iMRMC")

fileName <- system.file("extdata", "Froc.xlsx",
package = "RJafroc", mustWork = TRUE)
FrocDataXlsx <- DfReadDataFile(fileName, sequentialNames = TRUE)
```

DfSaveDataFile *Save ROC data file in a different format*

Description

Save ROC data file in a different format so it can be analyzed with alternate software

Usage

```
DfSaveDataFile(
  dataset,
  fileName,
  format = "JAFROC",
  dataDescription = paste0(deparse(substitute(dataset)), " Data File")
)
```

Arguments

dataset	The dataset to be saved in the specified format, see RJafroc-package.
fileName	The file name of the output data file. The extension of the data file must match the corresponding format, see RJafroc-package
format	The format of the data file, which can be "JAFROC", "MRMC" or "iMRMC", see RJafroc-package.
dataDescription	An optional string variable describing the data file, the default value is the variable name of dataset The description appears on the first line of *.lrc or *imrmc data file. This parameter is not used when saving dataset in other formats.

Examples

```
## DfSaveDataFile(dataset = dataset05,
##    fileName = "rocData2.xlsx", format = "JAFROC")
## DfSaveDataFile(dataset = dataset02,
##    fileName = "rocData2.csv", format = "MRMC")
## DfSaveDataFile(dataset = dataset02,
##    fileName = "rocData2.lrc", format = "MRMC",
##     dataDescription = "ExampleROCdata1")
## DfSaveDataFile(dataset = dataset02,
##    fileName = "rocData2.txt", format = "MRMC",
##     dataDescription = "ExampleROCdata2")
##  DfSaveDataFile(dataset = dataset02,
##    fileName = "dataset05.imrmc", format = "iMRMC",
##    dataDescription = "ExampleROCdata3")
```

`FitBinormalRoc` *Fit the binormal model to selected treatment and reader in an ROC dataset*

Description

Fit the binormal model-predicted ROC curve for a dataset. This is the R equivalent of ROCFIT or RSCORE

Usage

```
FitBinormalRoc(dataset, trt = 1, rdr = 1)
```

Arguments

`dataset`	The ROC dataset
`trt`	The desired treatment, default is 1
`rdr`	The desired reader, default is 1

Details

In the binormal model ratings (more accurately the latent decision variables) from diseased cases are sampled from $N(a, 1)$ while ratings for non-diseased cases are sampled from $N(0, b^2)$. To avoid clutter error bars are only shown for the lowest and uppermost operating points. An FROC dataset is internally converted to a highest rating inferred ROC dataset. To many bins containing zero counts will cause the algorithm to fail; so be sure to bin the data appropriately to fewer bins, where each bin has at least one count.

Value

The returned value is a list with the following elements:

a	The mean of the diseased distribution; the non-diseased distribution is assumed to have zero mean
b	The standard deviation of the non-diseased distribution. The diseased distribution is assumed to have unit standard deviation
zetas	The binormal model cutoffs, zetas or thresholds
AUC	The binormal model fitted ROC-AUC
StdAUC	The standard deviation of AUC
NLLIni	The initial value of negative LL
NLLFin	The final value of negative LL
ChisqrFitStats	The chisquare goodness of fit results
covMat	The covariance matrix of the parameters
fittedPlot	A **ggplot2** object containing the fitted operating characteristic along with the empirical operating points. Use `print()` to display the object

References

Dorfman DD, Alf E (1969) Maximum-Likelihood Estimation of Parameters of Signal-Detection Theory and Determination of Confidence Intervals - Rating-Method Data, Journal of Mathematical Psychology 6, 487-496.

Grey D, Morgan B (1972) Some aspects of ROC curve-fitting: normal and logistic models. Journal of Mathematical Psychology 9, 128-139.

Examples

```
## Test with an included ROC dataset
retFit <- FitBinormalRoc(dataset02);## print(retFit$fittedPlot)


## Test with an included FROC dataset; it needs to be binned
## as there are more than 5 discrete ratings levels
binned <- DfBinDataset(dataset05, desiredNumBins = 5, opChType = "ROC")
retFit <- FitBinormalRoc(binned);## print(retFit$fittedPlot)


## Test with single interior point data
fp <- c(rep(1,7), rep(2, 3))
tp <- c(rep(1,5), rep(2, 5))
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitBinormalRoc(dataset);## print(retFit$fittedPlot)

## Test with two interior data points
fp <- c(rep(1,7), rep(2, 5), rep(3, 3))
tp <- c(rep(1,3), rep(2, 5), rep(3, 7))
```

```
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitBinormalRoc(dataset);## print(retFit$fittedPlot)

## Test with TONY data for which chisqr can be calculated
ds <- DfFroc2Roc(dataset01)
retFit <- FitBinormalRoc(ds, 2, 3);## print(retFit$fittedPlot)
retFit$ChisqrFitStats

## Test with included degenerate ROC data
retFit <- FitBinormalRoc(datasetDegenerate);## print(retFit$fittedPlot)
```

`FitCbmRoc` *Fit the contaminated binormal model (CBM) to selected treatment and reader in an ROC dataset*

Description

Fit the CBM-predicted ROC curve for specified treatment and reader

Usage

```
FitCbmRoc(dataset, trt = 1, rdr = 1)
```

Arguments

`dataset`	The dataset containing the data
`trt`	The desired treatment, default is 1
`rdr`	The desired reader, default is 1

Details

In CBM ratings from diseased cases are sampled from a mixture distribution: (1) with integrated area $alpha$ distributed $N(\text{mu}1)$ and (2) from a distribution with integrated area $1-alpha$ distributed$N(0,1)$. Ratings for non-diseased cases are sampled from $N(0,1)$. The `ChisqrFitStats` consists of a list containing the chi-square value, the p-value and the degrees of freedom.

Value

The return value is a list with the following elements:

`mu`	The mean of the visible diseased distribution (the non-diseased) has zero mean
`alpha`	The proportion of diseased cases where the disease is visible
`zetas`	The cutoffs, zetas or thresholds

AUC	The AUC of the fitted ROC curve
StdAUC	The standard deviation of AUC
NLLIni	The initial value of negative LL
NLLFin	The final value of negative LL
ChisqrFitStats	The chisquare goodness of fit results
covMat	The covariance matrix of the parameters
fittedPlot	A **ggplot2** object containing the fitted operating characteristic along with the empirical operating points. Use `print()` to display the object

Note

This algorithm is more robust than the binormal model.

References

Dorfman DD, Berbaum KS (2000) A contaminated binormal model for ROC data: Part II. A formal model, Acad Radiol, 7:6, 427–437.

Examples

```
## CPU time 8.7 sec on Ubuntu (#13)
## Test with included ROC data
retFit <- FitCbmRoc(dataset02);## print(retFit$fittedPlot)

## Test with included degenerate ROC data (yes! CBM can fit such data)
retFit <- FitCbmRoc(datasetDegenerate);## print(retFit$fittedPlot)

## Test with single interior point data
fp <- c(rep(1,7), rep(2, 3))
tp <- c(rep(1,5), rep(2, 5))
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitCbmRoc(dataset);## print(retFit$fittedPlot)

## Test with two interior data points
fp <- c(rep(1,7), rep(2, 5), rep(3, 3))
tp <- c(rep(1,3), rep(2, 5), rep(3, 7))
dataset <- Df2RJafrocDataset(fp, tp)
retFit <- FitCbmRoc(dataset);
## print(retFit$fittedPlot)

## Test with included ROC data (some bins have zero counts)
retFit <- FitCbmRoc(dataset02, 2, 1);## print(retFit$fittedPlot)

## Test with TONY data for which chisqr can be calculated
ds <- DfFroc2Roc(dataset01)
retFit <- FitCbmRoc(ds, 2, 3);## print(retFit$fittedPlot)
retFit$ChisqrFitStats
```

FitCorCbm *Fit CORCBM to a paired ROC dataset*

Description

Fit the Correlated Contaminated Binormal Model (CORCBM) to a paired ROC dataset. The **ROC** dataset has to be formatted as a **single treatment**, **two-reader** dataset, even though the actual pairing may be different, see details.

Usage

```
FitCorCbm(dataset)
```

Arguments

dataset	A **paired ROC** dataset

Details

The conditions (X, Y) can be two readers interpreting images in the same treatment, the same reader interpreting images in different treatments, or different readers interpreting images in 2 different treatments. Function DfExtractCorCbmDataset can be used to construct a dataset suitable for FitCorCbm. With reference to the returned values, and assuming R bins in condition X and L bins in conditon Y, FPCounts is the R x L matrix containing the counts for non-diseased cases, TPCounts is the R x L matrix containing the counts for diseased cases; muX,muY,alphaX,alphaY,rhoNor,rhoAbn2 are the CORCBM parameters; aucX,aucX are the AUCs in the two conditions; stdAucX,stdAucY are the corresponding standard errors;stdErr contains the standard errors of the parameters of the model; areaStat, areaPval,covMat are the area-statistic, the p-value and the covariance matrix of the parameters. If a parameter approaches a limit, e.g., rhoNor = 0.9999, it is held constant at near the limiting value and the covariance matrix has one less dimension (along each edge) for each parameter that is held constant. The indices of the parameters held fixed are in fitCorCbmRet$fixParam.

Value

The return value is a list containing three objects:

fitCorCbmRet	list(FPCounts,TPCounts, muX,muY,alphaX,alphaY,rhoNor, rhoAbn2,zetaX,zetaY,covMat,fixParam)
stats	list(aucX,aucX,stdAucX, stdAucY,stdErr,areaStat,areaPval)
fittedPlot	The fitted plot with operating points, error bars, for both conditions

References

Zhai X, Chakraborty DP (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

FitRsmRoc *Fit the radiological search model (RSM) to an ROC dataset*

Description

Fit an RSM-predicted ROC curve to a **binned single-modality single-treatment ROC dataset**

Usage

```
FitRsmRoc(binnedRocData, lesDistr, trt = 1, rdr = 1)
```

Arguments

binnedRocData	The **binned ROC** dataset containing the data
lesDistr	The lesion distribution 1D array.
trt	The selected treatment, default is 1
rdr	The selected reader, default is 1

Details

If dataset is FROC, first convert it to ROC, using DfFroc2Roc. MLE ROC algorithms require binned datasets. Use DfBinDataset to perform the binning prior to calling this function. In the RSM: (1) The (random) number of latent NLs per case is Poisson distributed with mean parameter lambdaP, and the corresponding ratings are sampled from $N(0,1)$. The (2) The (random) number of latent LLs per diseased case is binomial distributed with success probability nuP and trial size equal to the number of lesions in the case, and the corresponding ratings are sampled from N(mu,1). (3) A latent NL or LL is actually marked if its rating exceeds the lowest threshold zeta1. To avoid clutter error bars are only shown for the lowest and uppermost operating points. Because of the extra parameter, and the requirement to have five counts, the chi-square statistic often cannot be calculated.

Value

The return value is a list with the following elements:

mu	The mean of the diseased distribution relative to the non-diseased one
lambdP	The Poisson parameter describing the distribution of latent NLs per case
nuP	The binomial success probability describing the distribution of latent LLs per diseased case
zetas	The RSM cutoffs, zetas or thresholds
AUC	The RSM fitted ROC-AUC
StdAUC	The standard deviation of AUC
NLLIni	The initial value of negative LL
NLLFin	The final value of negative LL

ChisqrFitStats	The chisquare goodness of fit results
covMat	The covariance matrix of the parameters
fittedPlot	A **ggplot2** object containing the fitted operating characteristic along with the empirical operating points. Use print to display the object

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm. Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search. Phys Med Biol 51, 3463–3482.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
## Test with included ROC data (some bins have zero counts)
lesDistr <- UtilLesionDistr(dataset02)
retFit <- FitRsmRoc(dataset02, lesDistr[,2])
## print(retFit$fittedPlot)

## Test with included degenerate ROC data
lesDistr <- UtilLesionDistr(datasetDegenerate)
retFit <- FitRsmRoc(datasetDegenerate, lesDistr[,2])

## Test with single interior point data
fp <- c(rep(1,7), rep(2, 3))
tp <- c(rep(1,5), rep(2, 5))
binnedRocData <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistr(binnedRocData)
retFit <- FitRsmRoc(binnedRocData, lesDistr[,2])

## Test with two interior data points
fp <- c(rep(1,7), rep(2, 5), rep(3, 3))
tp <- c(rep(1,3), rep(2, 5), rep(3, 7))
binnedRocData <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistr(binnedRocData)
retFit <- FitRsmRoc(binnedRocData, lesDistr[,2])


## Test with three interior data points
fp <- c(rep(1,12), rep(2, 5), rep(3, 3), rep(4, 5)) #25
tp <- c(rep(1,3), rep(2, 5), rep(3, 7), rep(4, 10)) #25
binnedRocData <- Df2RJafrocDataset(fp, tp)
lesDistr <- UtilLesionDistr(binnedRocData)
retFit <- FitRsmRoc(binnedRocData, lesDistr[,2])

## test for TONY data, i = 2 and j = 3
## only case permitting chisqure calculation
lesDistr <- UtilLesionDistr(dataset01)
```

```
rocData <- DfFroc2Roc(dataset01)
retFit <- FitRsmRoc(rocData, lesDistr[,2], trt = 2, rdr = 3)
## print(retFit$fittedPlot)
retFit$ChisqrFitStats
```

`isBinnedDataset` *Determine if a dataset is binned*

Description

Determine if a dataset is binned

Usage

```
isBinnedDataset(dataset, maxUniqeRatings = 6)
```

Arguments

`dataset`	The dataset
`maxUniqeRatings`	For each treatment-reader combination, the max number of unique ratings in order to be classified as binned, the default value for `maxUniqeRatings` is 6; if there are more unique ratings the treatment-reader combination is classified as not binned.

Value

a logical `[I x J]` array, TRUE if the corresponding treatment-reader combination is binned, i.e., has at most `maxUniqeRatings` unique ratings, FALSE otherwise.

Examples

```
isBinnedDataset(dataset01)
```

isValidDataset *Check the validity of a dataset*

Description

Checks the validity of the dataset.

Usage

```
isValidDataset(dataset)
```

Arguments

dataset	The dataseet object to be checked.

Value

TRUE if dataset is valid, FALSE otherwise.

PlotBinormalFit *Plot binormal fit*

Description

Plot the binormal-predicted ROC curve with provided parameters

Usage

```
PlotBinormalFit(a, b)
```

Arguments

a	vector: the mean(s) of the diseased distribution(s).
b	vector: the standard deviations(s) of the diseased distribution(s).

Details

a and b must have the same length. The predicted ROC curve for each a and b pair will be plotted.

Value

A **ggplot2** object of the plotted ROC curve(s) are returned. Use print function to display the saved object.

Examples

```
binormalPlot <- PlotBinormalFit(c(1, 2), c(0.5, 0.5))
## print(binormalPlot)
```

`PlotCbmFit` *Plot CBM fitted curve*

Description

Plot the CBM-predicted ROC curve with provided CBM parameters

Usage

```
PlotCbmFit(mu, alpha)
```

Arguments

`mu`	vector: the mean(s) of the z-samples of the diseased distribution(s) where the disease is visible
`alpha`	vector: the proportion(s) of the diseased distribution(s) where the disease is visible

Details

`mu` and `alpha` must have equal length. The predicted ROC curve for each `mu` and `alpha` pair will be plotted.

Value

A **ggplot2** object of the plotted ROC curve(s)

References

Dorfman DD, Berbaum KS (2000) A contaminated binormal model for ROC data: Part II. A formal model, Acad Radiol 7, 427–437.

Examples

```
cbmPlot <- PlotCbmFit(c(1, 2), c(0.5, 0.5))
## print(cbmPlot)
```

`PlotEmpiricalOperatingCharacteristics` *Plot empirical operating characteristics, ROC, FROC or LROC*

Description

Plot empirical operating characteristics (operating points connected by straight lines) for specified modalities and readers, or, if desired, plots (no operating points) averaged over specified modalities and / or readers.

Usage

```
PlotEmpiricalOperatingCharacteristics(
  dataset,
  trts = 1,
  rdrs = 1,
  opChType,
  legend.position = c(0.8, 0.3),
  maxDiscrete = 10
)
```

Arguments

`dataset`	Dataset object.
`trts`	List or vector: **integer** indices of modalities to be plotted. Default is 1.
`rdrs`	List or vector: **integer** indices of readers to be plotted. Default is 1.
`opChType`	Type of operating characteristic to be plotted: `"ROC"`, `"FROC"`, `"AFROC"`, `"wAFROC"`, `"AFROC1"`, `"wAFROC1"`, or `"LROC"`.
`legend.position`	Where to position the legend. The default is c(0.8, 0.2), i.e., 0.8 rightward and 0.2 upward (the plot is a unit square).
`maxDiscrete`	maximum number of op. points in order to be considered discrete and to be displayed by symbols and connecting lines; any more points will be regarded as continuous and only connected by lines; default is 10.

Details

The `trts` and `rdrs` are vectors or lists of **integer** indices, not the corresponding **string** IDs. For example, if the string ID of the first reader is "0", the value in `rdrs` should be **1** not **0**. The legend will display the string IDs.

If both of `trts` and `rdrs` are vectors, all combinations of modalities and readers are plotted. See Example 1.

If both `trts` and `rdrs` are `lists`, they must have the same length. Only the combination of modality and reader at the same position in their respective lists are plotted. If some elements of the

modalities and / or readers lists are vectors, the average operating characteristic over the implied modalities and / or readers are plotted. See Example 2.

For LROC datasets, opChType can be "ROC" or "LROC".

Value

A **ggplot2** object containing the operating characteristic plot(s) and a data frame containing the points defining the operating characteristics.

Plot	**ggplot2** object. For continuous or averaged data, operating characteristics curves are plotted **without** showing operating points. For binned (individual) data, both operating points and connecting lines are shown. To avoid clutter, if there are more than 20 operating points, they are not shown.
Points	Data frame with four columns: abscissa, ordinate, class (which codes modality and reader names) and type, which can be "D" for discrete ratings, "C" for continuous ratings, i.e., more than 20 operating points, or "A", for reader averaged.

Examples

```
## Example 1
## Plot individual empirical ROC plots for all combinations of modalities
## 1 and 2 and readers 1, 2 and 3. Six operating characteristics are plotted.

ret <- PlotEmpiricalOperatingCharacteristics(dataset =
dataset02, trts = c(1:2), rdrs = c(1:3), opChType = "ROC")
## print(ret$Plot)

## Example 2
## Empirical wAFROC plots, consisting of
## three sub-plots:
## (1) sub-plot, red, with operating points, for the 1st modality (string ID "1") and the 2nd
## reader (string ID "3"), labeled "M:1 R:3"
## (2) sub-plot, green, no operating points, for the 2nd modality (string ID "2") AVERAGED
## over the 2nd and 3rd readers (string IDs "3" and "4"), labeled "M:2  R: 3 4"
## (3) sub-plot, blue, no operating points, AVERAGED over the first two modalities
## (string IDs "1" and "2") AND over the 1st, 2nd and 3rd readers
## (string IDs "1", "3" and "4"), labeled "M: 1 2  R: 1  3 4"

plotT <- list(1, 2, c(1:2))
plotR <- list(2, c(2:3), c(1:3))

ret <- PlotEmpiricalOperatingCharacteristics(dataset = dataset04, trts = plotT,
   rdrs = plotR, opChType = "wAFROC")
## print(ret$Plot)

## Example 3
## Correspondences between indices and string identifiers for modalities and
## readers in this dataset (apparently reader "2" did not complete the study).

## names(dataset04$descriptions$readerID)
## [1] "1" "3" "4" "5"
```

PlotRsmOperatingCharacteristics *RSM predicted operating characteristics, ROC highest rating pdfs and FOMs, for FROC data*

Description

Visualize RSM predicted ROC, AFROC, wAFROC, FROC and pdf (probability density functions of highest ratings curves for non-diseased and diseased cases), for sets of search model parameters: mu, lambda, nu and zeta1.

Usage

```
PlotRsmOperatingCharacteristics(
  mu,
  lambda,
  nu,
  zeta1,
  lesDistr,
  relWeights = 0,
  OpChType = "ALL",
  legendPosition = c(1, 0),
  legendDirection = "horizontal",
  legendJustification = c(0, 1),
  nlfRange = NULL,
  llfRange = NULL,
  nlfAlpha = NULL
)
```

Arguments

mu	Array: the mean of the Gaussian distribution for the ratings of latent LLs (continuous ratings of lesions that are found by the observer's search mechanism). The ratings of NLs are distributed as N(0,1).
lambda	Array: the *intrinsic* Poisson distribution parameter which models the random numbers of latent NLs (suspicious regions that do not correspond to actual lesions) per case. The corresponding *physical* parameter is `lambda/mu`. Two conversion functions are provided: `UtilIntrinsic2PhysicalRSM` and `UtilPhysical2IntrinsicRSM`.
nu	Array: the *intrinsic* parameter which models the random numbers of latent LLs (suspicious regions that correspond to actual lesions) per diseased case. The corresponding *physical* parameter is `1 -exp(nu*mu)`, the success probability of the binomial distribution.
zeta1	Array, the lowest reporting threshold; if missing the default is -3. [Used to demonstrate continuity of the slope of the ROC at the end point; TBA Online Appendix 17.H.3]

lesDistr	Array: the probability mass function of the lesion distribution for diseased cases. See UtilLesionDistr.
relWeights	The relative weights of the lesions; a vector of length equal to length(maxLL). The default is zero, in which case equal weights are assumed.
OpChType	The type of operating characteristic desired: can be "ROC", "AFROC", "wAFROC", "FROC" or "pdfs" or "ALL". The default is "ALL".
legendPosition	The positioning of the legend: "right", "left", "top" or "bottom". Use "none" to suppress the legend.
legendDirection	Allows control on the direction of the legend; "horizontal", the default, or "vertical"
legendJustification	Where to position the legend, default is bottom right corner c(0,1)
nlfRange	**This applies to FROC plot only**. The x-axis range, e.g., c(0,2), for FROC plot. Default is "NULL", which means the maximum NLF range, as determined by the data.
llfRange	**This applies to FROC plot only**. The y-axis range, e.g., c(0,1), for FROC plot. Default is "NULL", which means the maximum LLF range, as determined by the data.
nlfAlpha	Upper limit of the integrated area under the FROC plot. Default is "NULL", which means the maximum NLF range is used (i.e., lambda/mu). Attempt to integrate outside the maximum NLF will generate an error.

Details

RSM is the Radiological Search Model described in the book. This function is vectorized with respect to the first 4 arguments. For lesDistr the sum must be one. To indicate that all dis. cases contain 4 lesions, set lesDistr = c(0,0,0,1).

Value

A list of elements containing five **ggplot2** objects (ROCPlot, AFROCPlot wAFROCPlot, FROC-Plot and PDFPlot) and two area measures (each of which can have up to two elements), the area under the search model predicted ROC curves in up to two treatments, the area under the search model predicted AFROC curves in up to two treatments, the area under the search model predicted wAFROC curves in up to two treatments, the area under the search model predicted FROC curves in up to two treatments.

- ROCPlot The predicted ROC plots
- AFROCPlot The predicted AFROC plots
- wAFROCPlot The predicted wAFROC plots
- FROCPlot The predicted FROC plots
- PDFPlot The predicted pdf plots
- aucROC The predicted ROC AUCs
- aucAFROC The predicted AFROC AUCs
- aucwAFROC The predicted wAFROC AUCs
- aucFROC The predicted FROC AUCs

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Chakraborty, DP, Yoon, HJ (2008) Operating characteristics predicted by models for diagnostic tasks involving lesion localization, Med Phys, 35:2, 435.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples* (CRC Press, Boca Raton, FL).

Examples

```
## Following example is for mu = 2, lambda = 1, nu = 0.6, in one treatment and
## mu = 3, lambda = 1.5, nu = 0.8, in the other treatment. 20% of the diseased
## cases have a single lesion, 40% have two lesions, 10% have 3 lesions,
## and 30% have 4 lesions.
lesDistr <- c(0.2, 0.4, 0.1, 0.3)

PlotRsmOperatingCharacteristics(mu = c(2, 3), lambda = c(1, 1.5), nu = c(0.6, 0.8),
   lesDistr = lesDistr, legendPosition = "bottom", nlfRange = c(0, 1), llfRange = c(0, 1))
```

SimulateCorCbmDataset *Simulate paired binned data for testing FitCorCbm*

Description

Simulates single treatment 2-reader binned ROC dataset, simulated according to the CORCBM model, for the purpose of testing the fitting program FitCorCbm.

Usage

```
SimulateCorCbmDataset(
  seed = 123,
  K1 = 50,
  K2 = 50,
  desiredNumBins = 5,
  muX = 1.5,
  muY = 3,
  alphaX = 0.4,
  alphaY = 0.7,
  rhoNor = 0.3,
  rhoAbn2 = 0.8
)
```

Arguments

seed	The seed variable, default is 123; set to NULL for truly random seed
K1	The number of non-diseased cases, default is 50
K2	The number of diseased cases, default is 50
desiredNumBins	The desired number of bins; default is 5
muX	The CBM mu parameter in condition X
muY	The CBM mu parameter in condition Y
alphaX	The CBM alpha parameter in condition X
alphaY	The CBM alpha parameter in condition Y
rhoNor	The correlation of non-diseased case z-samples
rhoAbn2	The correlation of diseased case z-samples, when disease is visible in both conditions

Details

X and Y refer to the two arms of the pairing. muX and alphaX refer to the univariate CBM parameters in condition X, rhoNor is the correlation of ratings of non-diseased cases and rhoAbn2 is the correlation of ratings of diseased cases when disease is visible in both conditions. The ROC data is bined to 5 bins in each condition. See referenced publication.

Value

The return value is the desired dataset, suitable for testing FitCorCbm

References

Zhai X, Chakraborty DP (2017) A bivariate contaminated binormal model for robust fitting of proper ROC curves to a pair of correlated, possibly degenerate, ROC datasets. Medical Physics. 44(6):2207–2222.

Examples

```
dataset <- SimulateCorCbmDataset()


## this takes very long
## dataset <- SimulateCorCbmDataset(K1 = 5000, K2 = 5000)
```

`SimulateFrocDataset` *Simulates an MRMC uncorrelated FROC dataset using the RSM*

Description

Simulates an uncorrelated MRMC FROC dataset for specified numbers of readers and treatments

Usage

```
SimulateFrocDataset(mu, lambda, nu, zeta1, I, J, K1, K2, perCase, seed = NULL)
```

Arguments

`mu`	The mu parameter of the RSM
`lambda`	The intrinsic lambda parameter of the RSM (not the physical parameter)
`nu`	The intrinsic nu parameter of the RSM (not the physical parameter)
`zeta1`	The lowest reporting threshold
`I`	The number of treatments
`J`	The number of readers
`K1`	The number of non-diseased cases
`K2`	The number of diseased cases
`perCase`	A K2 length array containing the numbers of lesions per diseased case
`seed`	The initial seed for the random number generator, the default is `NULL`, as if no seed has been specified.

Details

See book chapters on the Radiological Search Model (RSM) for details. In this code correlations between ratings on the same case are assumed to be zero.

Value

The return value is an FROC dataset.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
set.seed(1)
K1 <- 5;K2 <- 7;
maxLL <- 2;perCase <- floor(runif(K2, 1, maxLL + 1))
mu <- 1;lambda <- 1;nu <- 1 ;zeta1 <- -1
I <- 2; J <- 5

frocDataRaw <- SimulateFrocDataset(
  mu = mu, lambda = lambda, nu = nu, zeta1 = zeta1,
  I = I, J = J, K1 = K1, K2 = K2, perCase = perCase )

## plot the data
ret <- PlotEmpiricalOperatingCharacteristics(frocDataRaw, opChType = "FROC")
## print(ret$Plot)
```

SimulateFrocFromLrocDataset

Simulates an "AUC-equivalent" FROC dataset from an LROC dataset

---

Description

Simulates a multiple-treatment multiple-reader "AUC-equivalent" FROC dataset from a supplied LROC dataset, e.g., datasetCadLroc.

Usage

```
SimulateFrocFromLrocDataset(dataset)
```

Arguments

`dataset`	The LROC dataset to be converted to FROC.

Details

The LROC paradigm always yields a single mark per case. Therefore the equivalent FROC will also have only one mark per case. The NL arrays of the two datasets are identical. The LL array is created by copying the LLCl array of the LROC dataset to the LL array of the FROC dataset, from diseased case index k2 = 1 to k2 = K2. Additionally, the LLIl array of the LROC dataset is copied to the NL array of the FROC dataset, starting at case index k1 = K1+1 to k1 = K1+K2. Any zero ratings are replace by -Infs. The equivalent FROC dataset has the same HrAuc as the original LROC dataset. See example. The main use of this function is to test the CAD significance testing functions using CAD FROC datasets, which I currently don't have.

Value

The equivalent FROC dataset

Examples

```
frocDataset <- SimulateFrocFromLrocDataset(datasetCadLroc)
lrocAuc <- UtilFigureOfMerit(datasetCadLroc, FOM = "Wilcoxon")
frocHrAuc <- UtilFigureOfMerit(frocDataset, FOM = "HrAuc")
```

SimulateLrocDataset *Simulates an uncorrelated FLROC FrocDataset using the RSM*

Description

Simulates an uncorrelated LROC dataset for specified numbers of readers and treatments

Usage

```
SimulateLrocDataset(mu, lambda, nu, zeta1, I, J, K1, K2, lesionVector)
```

Arguments

mu	The intrinsic mu parameter of the RSM
lambda	The intrinsic lambda parameter of the RSM (not the physical parameter)
nu	The intrinsic nu parameter of the RSM (not the physical parameter)
zeta1	The lowest reporting threshold
I	The number of treatments
J	The number of readers
K1	The number of non-diseased cases
K2	The number of diseased cases
lesionVector	A K2 length array containing the numbers of lesions per diseased case

Details

See book chapters on the Radiological Search Model (RSM) for details. The spproach is to first simulate an FROC dataset and then convert it to an Lroc dataset. The correlations between FROC ratings on the same case are assumed to be zero.

Value

The return value is an LROC dataset.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
set.seed(1)
K1 <- 5
K2 <- 5
mu <- 2
lambda <- 1
lesionVector <- rep(1, 5)
nu <- 0.8
zeta1 <- -3
frocData <- SimulateFrocDataset(mu, lambda, nu, zeta1, I = 2, J = 5, K1, K2, lesionVector)
lrocData <- DfFroc2Lroc(frocData)
```

`SimulateRocDataset` *Simulates a binormal model ROC dataset*

Description

Simulates an uncorrelated binormal model ROC factorial dataset

Usage

```
SimulateRocDataset(I = 1, J = 1, K1, K2, a, b, seed = NULL)
```

Arguments

`I`	The number of modalities, default is 1
`J`	The number of readers, default is 1
`K1`	The number of non-diseased cases
`K2`	The number of diseased cases
`a`	The a parameter of the binormal model
`b`	The b parameter of the binormal model
`seed`	The initial seed, default is NULL, which results in a random seed

Details

See book Chapter 6 for details

Value

An ROC dataset

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
K1 <- 5;K2 <- 7;a <- 1.5;b <- 0.5
rocDataRaw <- SimulateRocDataset(K1 = K1, K2 = K2, a = a, b = b)
```

SsFrocNhRsmModel *RSM fitted model for FROC sample size*

Description

RSM fitted model for FROC sample size

Usage

```
SsFrocNhRsmModel(dataset, lesDistr)
```

Arguments

dataset	The **pilot** dataset object representing a NH ROC (or FROC) dataset.
lesDistr	A 1D array containing the probability mass function of number of lesions per diseased case in the **pivotal FROC** study.

Details

If dataset is FROC, it is converted to an ROC dataset. The search model is used to fit each treatment-reader combination in the pilot dataset. The median value for each parameter is computed and are returned by the function (3 vaalues). These are used to compute predicted wAFROC and ROC FOMS over a range of values of deltaMu, which are fitted by a straight line constrained to pass throught the origin. The scaleFactor (scaling factor) and R2 are returned. The scaling factor is the value by which the ROC effect size must be multiplied to get the wAFROC effect size. Also returned are the lesDist and lesWghtDist arrays, which are needed for computing FOMs. See 2nd FROC SS vignette. Equally weighted lesions is assumed.

Value

A list containing:

- muMed, the median mu parameter of the NH model.
- lambdaMed, the median lambda parameter of the NH model.
- nuMed, the median nu parameter of the NH model.
- lesDistr, the lesion distribution 2D array.
- lesWghtDistr, the lesion weight distribution 2D array.
- scaleFactor, the scaling factor that multiplies the ROC effect size to get wAFROC effect size.
- R2, the R2 of the fit.

Examples

```
## Examples with CPU or elapsed time > 5s
## user system elapsed
## SsFrocNhRsmModel 8.102  0.023   8.135

## SsFrocNhRsmModel(dataset02, c(0.7, 0.2, 0.1))
## the next one should match the vignette
## SsFrocNhRsmModel(DfExtractDataset(dataset04, trts = c(1,2)), c(0.69, 0.2, 0.11))
```

`SsPowerGivenJK` *Statistical power for specified numbers of readers and cases*

Description

Calculate the statistical power for specified numbers of readers J, cases K, analysis method and DBM or OR variances components

Usage

```
SsPowerGivenJK(
  dataset,
  ...,
  FOM,
  J,
  K,
  effectSize = NULL,
  method = "OR",
  analysisOption = "RRRC",
  LegacyCode = FALSE,
  alpha = 0.05
)
```

Arguments

`dataset`	The **pilot** dataset. If set to NULL then variance components must be supplied.
`...`	Optional variance components. These are needed if `dataset` is not supplied.
`FOM`	The figure of merit
`J`	The number of readers in the pivotal study.
`K`	The number of cases in the pivotal study.
`effectSize`	The effect size to be used in the **pivotal** study. Default is NULL, which uses the observed effect size in the pilot dataset. Must be supplied if dataset is set to NULL and variance components are supplied.

method	"OR" (the default) or "DBM" (but see LegacyCode option below).
analysisOption	Desired generalization, "RRRC" (the default), "FRRC", "RRFC" or "ALL". RRFC = random reader fixed case, etc.
LegacyCode	Logical, defaults to FALSE, which results in OR sample size method being used, even if DBM method is specified, as in Hillis 2011 & 2018 papers. If TRUE the method based on Hillis-Berbaum 2004 sample size paper is used.
alpha	The significance level, default is 0.05.

Details

The default effectSize uses the observed effect size in the pilot study. A numeric value over-rides the default value. This argument must be supplied if dataset = NULL and variance compenents (the ... arguments) are supplied.

Value

The expected statistical power.

Note

The procedure is valid for ROC studies only; for FROC studies see Vignettes 19.

References

Hillis SL, Berbaum KS (2004). Power Estimation for the Dorfman-Berbaum-Metz Method. Acad Radiol, 11, 1260–1273.

Hillis SL, Obuchowski NA, Berbaum KS (2011). Power Estimation for Multireader ROC Methods: An Updated and Unified Approach. Acad Radiol, 18, 129–142.

Hillis SL, Schartz KM (2018). Multireader sample size program for diagnostic studies: demonstration and methodology. Journal of Medical Imaging, 5(04).

Examples

```
## EXAMPLE 1: RRRC power
## specify 2-treatment ROC dataset and force DBM alg.
SsPowerGivenJK(dataset = dataset02, FOM = "Wilcoxon", effectSize = 0.05,
J = 6, K = 251, method = "DBM", LegacyCode = TRUE) # RRRC is default

## EXAMPLE 1A: FRRC power
SsPowerGivenJK(dataset = dataset02, FOM = "Wilcoxon", effectSize = 0.05,
J = 6, K = 251, method = "DBM", LegacyCode = TRUE, analysisOption = "FRRC")

## EXAMPLE 1B: RRFC power
SsPowerGivenJK(dataset = dataset02, FOM = "Wilcoxon", effectSize = 0.05,
J = 6, K = 251, method = "DBM", LegacyCode = TRUE, analysisOption = "RRFC")

## EXAMPLE 2: specify NULL dataset & DBM var. comp. & force DBM-based alg.
vcDBM <- UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")$VarCom
SsPowerGivenJK(dataset = NULL, FOM = "Wilcoxon", J = 6, K = 251,
```

```
effectSize = 0.05, method = "DBM", LegacyCode = TRUE,
list(
VarTR = vcDBM["VarTR","Estimates"], # replace rhs with actual values as in 4A
VarTC = vcDBM["VarTC","Estimates"], # do:
VarErr = vcDBM["VarErr","Estimates"])) # do:

## EXAMPLE 3: specify 2-treatment ROC dataset and use OR-based alg.
SsPowerGivenJK(dataset = dataset02, FOM = "Wilcoxon", effectSize = 0.05,
J = 6, K = 251)

## EXAMPLE 4: specify NULL dataset & OR var. comp. & use OR-based alg.
JStar <- length(dataset02$ratings$NL[1,,1,1])
KStar <- length(dataset02$ratings$NL[1,1,,1])
vcOR <- UtilORVarComponentsFactorial(dataset02, FOM = "Wilcoxon")$VarCom
SsPowerGivenJK(dataset = NULL, FOM = "Wilcoxon", effectSize = 0.05, J = 6,
K = 251, list(JStar = JStar, KStar = KStar,
   VarTR = vcOR["VarTR","Estimates"], # replace rhs with actual values as in 4A
   Cov1 = vcOR["Cov1","Estimates"],   # do:
   Cov2 = vcOR["Cov2","Estimates"],   # do:
   Cov3 = vcOR["Cov3","Estimates"],   # do:
   Var = vcOR["Var","Estimates"]))

## EXAMPLE 4A: specify NULL dataset & OR var. comp. & use OR-based alg.
SsPowerGivenJK(dataset = NULL, FOM = "Wilcoxon", effectSize = 0.05, J = 6,
K = 251, list(JStar = 5, KStar = 114,
   VarTR = 0.00020040252,
   Cov1 = 0.00034661371,
   Cov2 = 0.00034407483,
   Cov3 = 0.00023902837,
   Var = 0.00080228827))

## EXAMPLE 5: specify NULL dataset & DBM var. comp. & use OR-based alg.
## The DBM var. comp. are converted internally to OR var. comp.
vcDBM <- UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")$VarCom
KStar <- length(dataset02$ratings$NL[1,1,,1])
SsPowerGivenJK(dataset = NULL, J = 6, K = 251, effectSize = 0.05,
method = "DBM", FOM = "Wilcoxon",
list(KStar = KStar,                # replace rhs with actual values as in 5A
VarR = vcDBM["VarR","Estimates"], # do:
VarC = vcDBM["VarC","Estimates"], # do:
VarTR = vcDBM["VarTR","Estimates"], # do:
VarTC = vcDBM["VarTC","Estimates"], # do:
VarRC = vcDBM["VarRC","Estimates"], # do:
VarErr = vcDBM["VarErr","Estimates"]))

## EXAMPLE 5A: specify NULL dataset & DBM var. comp. & use OR-based alg.
SsPowerGivenJK(dataset = NULL, J = 6, K = 251, effectSize = 0.05,
method = "DBM", FOM = "Wilcoxon",
list(KStar = 114,
VarR = 0.00153499935,
VarC = 0.02724923428,
VarTR = 0.00020040252,
VarTC = 0.01197529621,
```

```
VarRC = 0.01226472859,
VarErr = 0.03997160319))
```

`SsPowerGivenJKDbmVarCom`

Power given J, K and Dorfman-Berbaum-Metz variance components

---

Description

Power given J, K and Dorfman-Berbaum-Metz variance components

Usage

```
SsPowerGivenJKDbmVarCom(
  J,
  K,
  effectSize,
  VarTR,
  VarTC,
  VarErr,
  alpha = 0.05,
  analysisOption = "RRRC"
)
```

Arguments

`J`	The number of readers
`K`	The number of cases
`effectSize`	The effect size
`VarTR`	The treatment-reader DBM variance component
`VarTC`	The treatment-case DBM variance component
`VarErr`	The error-term DBM variance component
`alpha`	The size of the test (default = 0.05)
`analysisOption`	The desired generalization ("RRRC", "FRRC", "RRFC", "ALL")

Details

The variance components are obtained using StSignificanceTesting with `method = "DBM"`.

Value

A list object containing the estimated power and associated statistics for each desired generalization.

Examples

```
VarCom <- StSignificanceTesting(dataset02, FOM = "Wilcoxon", method = "DBM",
   analysisOption = "RRRC")$ANOVA$VarCom
VarTR <- VarCom["VarTR",1]
VarTC <- VarCom["VarTC",1]
VarErr <- VarCom["VarErr",1]
ret <- SsPowerGivenJKDbmVarCom (J = 5, K = 100, effectSize = 0.05, VarTR,
   VarTC, VarErr, analysisOption = "RRRC")
cat("RRRC power = ", ret$powerRRRC)
```

SsPowerGivenJKOrVarCom

Power given J, K and Obuchowski-Rockette variance components

Description

Power given J, K and Obuchowski-Rockette variance components

Usage

```
SsPowerGivenJKOrVarCom(
  J,
  K,
  KStar,
  effectSize,
  VarTR,
  Cov1,
  Cov2,
  Cov3,
  Var,
  alpha = 0.05,
  analysisOption = "RRRC"
)
```

Arguments

J	The number of readers in the **pivotal** study
K	The number of cases in the **pivotal** study
KStar	The number of cases in the **pilot** study
effectSize	The effect size
VarTR	The treatment-reader OR variance component
Cov1	The OR Cov1 covariance
Cov2	The OR Cov2 covariance
Cov3	The OR Cov3 covariance

Var	The OR pure variance term
alpha	The size of the test (default = 0.05)
analysisOption	The desired generalization ("RRRC", "FRRC", "RRFC", "ALL")

Details

The variance components are obtained using StSignificanceTesting with method = "OR".

Value

A list object containing the estimated power and associated statistics for each desired generalization.

Examples

```
dataset <- dataset02 ## the pilot study
KStar <- length(dataset$ratings$NL[1,1,,1])
VarCom <- StSignificanceTesting(dataset, FOM = "Wilcoxon",
method = "OR", analysisOption = "RRRC")$ANOVA$VarCom
VarTR <- VarCom["VarTR",1]
Cov1 <- VarCom["Cov1",1]
Cov2 <- VarCom["Cov2",1]
Cov3 <- VarCom["Cov3",1]
Var <- VarCom["Var",1]
ret <- SsPowerGivenJKOrVarCom (J = 5, K = 100, KStar = KStar,
   effectSize = 0.05, VarTR, Cov1, Cov2, Cov3, Var, analysisOption = "RRRC")

cat("RRRC power = ", ret$powerRRRC)
```

SsPowerTable *Generate a power table using the OR method*

Description

Generate combinations of numbers of readers J and numbers of cases K for desired power and specified generalization(s)

Usage

```
SsPowerTable(
  dataset,
  FOM,
  effectSize = NULL,
  alpha = 0.05,
  desiredPower = 0.8,
  analysisOption = "RRRC"
)
```

Arguments

dataset	The **pilot** ROC dataset to be used to extrapolate to the **pivotal** study.
FOM	The figure of merit.
effectSize	The effect size to be used in the **pivotal** study, default value is NULL. See Details.
alpha	The The size of the test, default is 0.05.
desiredPower	The desired statistical power, default is 0.8.
analysisOption	Desired generalization, "RRRC" (the default), "FRRC", "RRFC" or "ALL".

Details

The default effectSize uses the observed effect size in the pilot study. A supplied numeric value over-rides the default value.

Value

A list containing up to 3 (depending on analysisOption) dataframes. Each dataframe contains 3 arrays:

numReaders	The numbers of readers in the pivotal study.
numCases	The numbers of cases in the pivotal study.
power	The estimated statistical powers.

Note

The procedure is valid for ROC studies only; for FROC studies see Vignettes 19.

Examples

```
## Examples with CPU or elapsed time > 5s
##              user    system elapsed
## SsPowerTable 20.033  0.037  20.077

## Example of sample size calculation with OR method
## SsPowerTable(dataset02, FOM = "Wilcoxon", method = "OR")
```

SsSampleSizeKGivenJ *Number of cases, for specified number of readers, to achieve desired power*

Description

Number of cases to achieve the desired power, for specified number of readers J, and specified DBM or ORH analysis method

Usage

```
SsSampleSizeKGivenJ(
  dataset,
  ...,
  J,
  FOM,
  effectSize = NULL,
  method = "OR",
  alpha = 0.05,
  desiredPower = 0.8,
  analysisOption = "RRRC",
  LegacyCode = FALSE
)
```

Arguments

dataset	The **pilot** dataset. If set to NULL then variance components must be supplied.
...	Optional variance components, VarTR, VarTC and VarErr. These are needed if dataset is not supplied.
J	The number of readers in the **pivotal** study.
FOM	The figure of merit. Not needed if variance components are supplied.
effectSize	The effect size to be used in the **pivotal** study. Default is NULL. Must be supplied if dataset is set to NULL and variance components are supplied.
method	"OR" (default) or "DBM".
alpha	The significance level of the study, default is 0.05.
desiredPower	The desired statistical power, default is 0.8.
analysisOption	Desired generalization, "RRRC", "FRRC", "RRFC" or "ALL" (the default).
LegacyCode	Logical, default is FALSE, if TRUE the DBM method is used. Otherwise the OR method is used.

Details

effectSize = NULL uses the **observed** effect size in the pilot study. A numeric value over-rides the default value. This argument must be supplied if dataset = NULL and variance compenents (the optional ... arguments) are supplied.

Value

A list of two elements:

K	The minimum number of cases K in the pivotal study to just achieve the desired statistical power, calculated for each value of analysisOption.
power	The predicted statistical power.

Note

The procedure is valid for ROC studies only; for FROC studies see Vignettes 19.

Examples

```
## the following two should give identical results
SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", effectSize = 0.05, J = 6, method = "DBM")

a <- UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")$VarCom
SsSampleSizeKGivenJ(dataset = NULL, J = 6, effectSize = 0.05, method = "DBM", LegacyCode = TRUE,
   list(VarTR = a["VarTR",1],
   VarTC = a["VarTC",1],
   VarErr = a["VarErr",1]))

## the following two should give identical results
SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", effectSize = 0.05, J = 6, method = "OR")

a <- UtilORVarComponentsFactorial(dataset02, FOM = "Wilcoxon")$VarCom
KStar <- length(dataset02$ratings$NL[1,1,,1])
SsSampleSizeKGivenJ(dataset = NULL, J = 6, effectSize = 0.05, method = "OR",
   list(KStar = KStar,
   VarTR = a["VarTR",1],
   Cov1 = a["Cov1",1],
   Cov2 = a["Cov2",1],
   Cov3 = a["Cov3",1],
   Var = a["Var",1]))


for (J in 6:10) {
 ret <- SsSampleSizeKGivenJ(dataset02, FOM = "Wilcoxon", J = J, analysisOption = "RRRC")
 message("# of readers = ", J, " estimated # of cases = ", ret$K,
 ", predicted power = ", signif(ret$powerRRRC,3), "\n")
}
```

StSignificanceTesting *Performs DBM or OR significance testing for factorial or split-plot A,C datasets*

Description

Performs Dorfman-Berbaum-Metz (DBM) or Obuchowski-Rockette (OR) significance testing, for specified dataset; significance testing refers to analysis designed to assign a P-value, and other statistics, for rejecting the null hypothesis (NH) that the reader-averaged figure of merit (FOM) differences between treatments is zero. The results of the analysis are best visualized in the text or Excel-formatted files produced by `UtilOutputReport`.

Usage

```
StSignificanceTesting(
  dataset,
  FOM,
  FPFValue = 0.2,
  alpha = 0.05,
  method = "DBM",
  covEstMethod = "jackknife",
  nBoots = 200,
  analysisOption = "ALL",
  tempOrgCode = FALSE
)
```

Arguments

`dataset`	The dataset to be analyzed, see `RJafroc-package`. Must have two or more treatments and two or more readers. The dataset design can be "FCTRL", "SPLIT-PLOT-A" or "SPLIT-PLOT-C".
`FOM`	The figure of merit, see `UtilFigureOfMerit`
`FPFValue`	Only needed for `LROC` data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
`alpha`	The significance level of the test of the null hypothesis that all treatment effects are zero; the default is 0.05
`method`	The significance testing method to be used: `"DBM"` (the default) or `"OR"`, representing the Dorfman-Berbaum-Metz and the Obuchowski-Rockette significance testing methods, respectively.
`covEstMethod`	The covariance matrix estimation method in `ORH` analysis (for `method = "DBM"` the jackknife is always used). • `"Jackknife"`, the default, • `"Bootstrap"`, in which case `nBoots` (above) is relevant, • `"DeLong"`; requires `FOM = "Wilcoxon" or "ROI" or "HrAuc"`, otherwise an error results.
`nBoots`	The number of bootstraps (defaults to 200), relevant only if `covEstMethod = "bootstrap"` and `method = "OR"`
`analysisOption`	Determines which factors are regarded as random vs. fixed: • `"RRRC"` = random-reader random case, • `"FRRC"` = fixed-reader random case,

- "RRFC" = random-reader fixed case,
- "ALL" = outputs results of "RRRC", "FRRC" and "RRFC" analyses - this is the default.

tempOrgCode, default FALSE; if TRUE, then code from version 0.0.1 of RJafroc is used (see RJafroc_0.0.1.tar). This is intended to check against errors that crept in subsequent to the original version as I attempted to improve the organization of the code and the output. As implicit in the name of this temporary flag, it will eventually be removed.

Value

For method = "DBM" **the returned list contains 4 dataframes:**

FOMs	Contains foms, trtMeans and trtMeanDiffs: see return of UtilFigureOfMerit
ANOVA	Contains TRCAnova, VarCom, IndividualTrt and IndividualRdr ANOVA tables of pseudovalues
RRRC	Contains results of "RRRC" analyses: FTests, ciDiffTrt, ciAvgRdrEachTrt
FRRC	Contains results of "FRRC" analyses: FTests, ciDiffTrt, ciAvgRdrEachTrt, ciDiffTrtEachRdr
RRFC	Contains results of "RRFC" analyses: FTests, ciDiffTrt, ciAvgRdrEachTrt

For method = "OR" **the return list contains 4 dataframes:**

FOMs	Contains foms, trtMeans and trtMeanDiffs: UtilFigureOfMerit
ANOVA	Contains TRAnova, VarCom, IndividualTrt and IndividualRdr ANOVA tables of FOM values
RRRC	Contains results of "RRRC" analyses - same organization as DBM, see above
FRRC	Contains results of "FRRC" analyses - ditto
RRFC	Contains results of "RRFC" analyses- ditto

References

Dorfman DD, Berbaum KS, Metz CE (1992) ROC characteristic rating analysis: Generalization to the Population of Readers and Patients with the Jackknife method, Invest. Radiol. 27, 723-731.

Obuchowski NA, Rockette HE (1995) Hypothesis Testing of the Diagnostic Accuracy for Multiple Diagnostic Tests: An ANOVA Approach with Dependent Observations, Communications in Statistics: Simulation and Computation 24, 285-308.

Hillis SL (2014) A marginal-mean ANOVA approach for analyzing multireader multicase radiological imaging data, Statistics in medicine 33, 330-360.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
StSignificanceTesting(dataset02,FOM = "Wilcoxon", method = "DBM")
StSignificanceTesting(dataset02,FOM = "Wilcoxon", method = "OR")
## following is split-plot-c analysis using a simulated split-plot-c dataset
StSignificanceTesting(datasetFROCSpC, FOM = "wAFROC", method = "OR")


StSignificanceTesting(dataset05, FOM = "wAFROC")
StSignificanceTesting(dataset05, FOM = "HrAuc", method = "DBM")
StSignificanceTesting(dataset05, FOM = "SongA1", method = "DBM")
StSignificanceTesting(dataset05, FOM = "SongA2", method = "DBM")
StSignificanceTesting(dataset05, FOM = "wAFROC1", method = "DBM")
StSignificanceTesting(dataset05, FOM = "AFROC1", method = "DBM")
StSignificanceTesting(dataset05, FOM = "AFROC", method = "DBM")
```

StSignificanceTestingCadVsRad

Significance testing: standalone CAD vs. radiologists

Description

Comparing standalone CAD vs. a group of radiologists interpreting the same cases; (ideally) **standalone CAD** means that all the **designer-level** mark-rating pairs provided by the CAD algorithm are available, not just the one or two marks usually displayed to the radiologist. At the very minimum, location-level information, such as in the LROC paradigm, should be used. Ideally the FROC paradigm should be used. A severe statistical power penalty is paid if one uses the ROC paradigm. Details of the method are in a pdf file that will be uploaded to GitHub and in my 2017 book.

Usage

```
StSignificanceTestingCadVsRad(
  dataset,
  FOM,
  FPFValue = 0.2,
  method = "1T-RRRC",
  alpha = 0.05,
  plots = FALSE
)
```

Arguments

dataset	**The dataset to be analzed; must be single-treatment multiple-readers, where the first reader is CAD.**

FOM	The desired FOM; for ROC data it must be "Wilcoxon", for FROC data it can be any valid FOM, e.g., "HrAuc", "wAFROC", etc; for LROC data it must be "Wilcoxon", or "PCL" or "ALROC".
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
method	The desired analysis: "1T-RRFC","1T-RRRC" (the default) or "2T-RRRC", see manuscript for details.
alpha	Significance level of the test, defaults to 0.05.
plots	Flag, default is FALSE, i.e., a plot is not displayed. If TRUE, it displays the appropriate operating characteristic for all readers and CAD.

Details

- **PCL** is the probability of a correct localization.
- The LROC is the plot of PCL (ordinate) vs. FPF.
- For LROC data, FOM = "PCL" means the interpolated PCL value at the specified FPFValue.
- For FOM = "ALROC" the trapezoidal area under the LROC from FPF = 0 to FPF = FPFValue is used.
- If method = "1T-RRRC" the first **reader** is assumed to be CAD.
- If method = "2T-RRRC" the first **treatment** is assumed to be CAD.
- The NH is that the FOM of CAD equals the average of the readers.
- The method = "1T-RRRC" analysis uses an adaptation of the single-treatment multiple-reader Obuchowski Rockette (OR) model described in a paper by Hillis (2007), section 5.3. It is characterized by 3 parameters VarR, Var and Cov2, where the latter two are estimated using the jackknife.
- For method = "2T-RRRC" the analysis replicates the CAD data as many times as necessary so as to form one "treatment" of an MRMC pairing, the other "treatment" being the radiologists. Then standard ORH analysis is applied. The method is described in Kooi et al. It gives exactly the same final results (F-statistic, ddf and p-value) as "1T-RRRC" but the intermediate quantities are meaningless.

Value

If method = "1T-RRRC" the return value is a list with the following elements:

fomCAD	The observed FOM for CAD.
fomRAD	The observed FOM array for the readers.
avgRadFom	The average FOM of the readers.
avgDiffFom	The mean of the difference FOM, RAD - CAD.
ciAvgDiffFom	The 95-percent CI of the average difference, RAD - CAD.
varR	The variance of the radiologists.
varError	The variance of the error term in the single-treatment multiple-reader OR model.
cov2	The covariance of the error term.

tstat	The observed value of the t-statistic; it's square is equivalent to an F-statistic.
df	The degrees of freedom of the t-statistic.
pval	The p-value for rejecting the NH.
Plots	If argument plots = TRUE, a **ggplot** object containing empirical operating characteristics corresponding to specified FOM. For example, if FOM = "Wilcoxon" an ROC plot object is produced where reader 1 is CAD. If an LROC FOM is selected, an LROC plot is displayed.

If method = "2T-RRRC" the return value is a list with the following elements:

fomCAD	The observed FOM for CAD.
fomRAD	The observed FOM array for the readers.
avgRadFom	The average FOM of the readers.
avgDiffFom	The mean of the difference FOM, RAD - CAD.
ciDiffFom	A data frame containing the statistics associated with the average difference, RAD - CAD.
ciAvgRdrEachTrt	A data frame containing the statistics associated with the average FOM in each "treatment".
varR	The variance of the pure reader term in the OR model.
varTR	The variance of the treatment-reader term error term in the OR model.
cov1	The covariance1 of the error term - same reader, different treatments.
cov2	The covariance2 of the error term - different readers, same treatment.
cov3	The covariance3 of the error term - different readers, different treatments.
varError	The variance of the pure error term in the OR model.
FStat	The observed value of the F-statistic.
ndf	The numerator degrees of freedom of the F-statistic.
df	The denominator degrees of freedom of the F-statistic.
pval	The p-value for rejecting the NH.
Plots	see above.

References

Hillis SL (2007) A comparison of denominator degrees of freedom methods for multiple observer ROC studies, Statistics in Medicine. 26:596-619.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Hupse R, Samulski M, Lobbes M, et al (2013) Standalone computer-aided detection compared to radiologists performance for the detection of mammographic masses, Eur Radiol. 23(1):93-100.

Kooi T, Gubern-Merida A, et al. (2016) A comparison between a deep convolutional neural network and radiologists for classifying regions of interest in mammography. Paper presented at: International Workshop on Digital Mammography, Malmo, Sweden.

Examples

```
ret1M <- StSignificanceTestingCadVsRad (dataset09,
FOM = "Wilcoxon", method = "1T-RRRC")

StSignificanceTestingCadVsRad(datasetCadLroc,
FOM = "Wilcoxon", method = "1T-RRFC")

retLroc1M <- StSignificanceTestingCadVsRad (datasetCadLroc,
FOM = "PCL", method = "1T-RRRC", FPFValue = 0.05)

## test with fewer readers
dataset09a <- DfExtractDataset(dataset09, rdrs = seq(1:7))
ret1M7 <- StSignificanceTestingCadVsRad (dataset09a,
FOM = "Wilcoxon", method = "1T-RRRC")

datasetCadLroc7 <- DfExtractDataset(datasetCadLroc, rdrs = seq(1:7))
ret1MLroc7 <- StSignificanceTestingCadVsRad (datasetCadLroc7,
FOM = "PCL", method = "1T-RRRC", FPFValue = 0.05)


## takes longer than 5 sec on OSX
## retLroc2M <- StSignificanceTestingCadVsRad (datasetCadLroc,
## FOM = "PCL", method = "2T-RRRC", FPFValue = 0.05)

## ret2MLroc7 <- StSignificanceTestingCadVsRad (datasetCadLroc7,
## FOM = "PCL", method = "2T-RRRC", FPFValue = 0.05)
```

StSignificanceTestingCrossedModalities

Perform significance testing using crossed treatments analysis

---

Description

Performs ORH analysis for specified crossed treatments dataset averaged over specified treatment factor

Usage

```
StSignificanceTestingCrossedModalities(
  ds,
  avgIndx,
  FOM = "wAFROC",
  alpha = 0.05,
  analysisOption = "ALL"
)
```

Arguments

ds	The crossed treatments dataset
avgIndx	The index of the treatment to be averaged over
FOM	See StSignificanceTesting
alpha	See StSignificanceTesting
analysisOption	See StSignificanceTesting

Value

The return list contains the same items with StSignificanceTesting.

Examples

```
## read the built in dataset
retCrossed2 <- StSignificanceTestingCrossedModalities(datasetCrossedModality, 1)
```

UtilAnalyticalAucsRSM *RSM ROC/AFROC/wAFROC AUC calculator*

Description

Returns the ROC, AFROC and wAFROC AUCs corresponding to specified RSM parameters. See also UtilAucPROPROC, UtilAucBinormal and UtilAucCBM

Usage

```
UtilAnalyticalAucsRSM(mu, lambda, nu, zeta1 = -Inf, lesDistr, relWeights = 0)
```

Arguments

mu	The mean of the Gaussian distribution for the ratings of latent LLs (continuous ratings of lesions that are found by the search mechanism). The NLs are assumed to be distributed as N(0,1).
lambda	The *intrinsic* Poisson distribution parameter, which describes the random number of latent NLs (suspicious regions that do not correspond to actual lesions) per case.
nu	The *intrinsic* nu parameters, the success probability of the binomial distribution describing the random numbers of latent LLs (suspicious regions that correspond to actual lesions) per diseased case.
zeta1	The lowest reporting threshold, the default is -Inf.
lesDistr	The lesion distribution 1D array, i.e., the probability mass function (pmf) of the numbers of lesions for diseased cases.
relWeights	The relative weights of the lesions; a vector of length maxLL; if zero, the default, equal weights are assumed.

Value

A list containing the ROC, AFROC and wAFROC AUCs corresponding to the specified parameters

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Examples

```
mu <- 1;lambda <- 1;nu <- 1
lesDistr <- c(0.9, 0.1)
## i.e., 90% of dis. cases have one lesion, and 10% have two lesions
relWeights <- c(0.05, 0.95)
## i.e., lesion 1 has weight 5 percent while lesion two has weight 95 percent

UtilAnalyticalAucsRSM(mu, lambda, nu, zeta1 = -Inf, lesDistr)
UtilAnalyticalAucsRSM(mu, lambda, nu, zeta1 = -Inf, lesDistr, relWeights)
```

UtilAucBinormal *Binormal model AUC function*

Description

Returns the Binormal model ROC-AUC corresponding to specified parameters. See also UtilAnalyticalAucsRSM, UtilAucPROPROC and UtilAucCBM

Usage

```
UtilAucBinormal(a, b)
```

Arguments

a	The a parameter of the binormal model (separation of non-diseased and diseased pdfs)
b	The b parameter of the binormal model (std. dev. of non-diseased diseased pdf; diseased pdf has unit std. dev)

Value

Binormal model-predicted ROC-AUC

References

Dorfman DD, Alf E (1969) Maximum-Likelihood Estimation of Parameters of Signal-Detection Theory and Determination of Confidence Intervals - Rating-Method Data, Journal of Mathematical Psychology. 6:487-496.

Examples

```
a <- 2;b <- 0.7
UtilAucBinormal(a,b)
```

`UtilAucCBM` *CBM AUC function*

Description

Returns the CBM ROC-AUC See also `UtilAnalyticalAucsRSM`, `UtilAucPROPROC` and `UtilAucBinormal`

Usage

```
UtilAucCBM(mu, alpha)
```

Arguments

`mu`	The `mu` parameter of CBM (separation of non-diseased and diseased pdfs)
`alpha`	The `alpha` parameter of CBM, i.e., the fraction of diseased cases on which the disease is visible

Value

CBM-predicted ROC-AUC for the specified parameters

References

Dorfman DD, Berbaum KS (2000) A contaminated binormal model for ROC data: Part II. A formal model, Acad Radiol 7:6 427–437.

Examples

```
mu <- 2;alpha <- 0.8
UtilAucCBM(mu,alpha)
```

UtilAucPROPROC *PROPROC AUC function*

Description

Returns the PROPROC ROC-AUC corresponding to specified parameters. See also UtilAnalyticalAucsRSM, UtilAucBinormal and UtilAucCBM

Usage

```
UtilAucPROPROC(c1, da)
```

Arguments

c1	The c-parameter of the PROPROC model, since **c is a reserved function in R**.
da	The da-parameter of the PROPROC model.

Value

PROPROC model-predicted ROC-AUC for the specified parameters

References

Metz CE, Pan X (1999) Proper Binormal ROC Curves: Theory and Maximum-Likelihood Estimation, J Math Psychol 43(1):1-33.

Examples

```
c1 <- .2;da <- 1.5
UtilAucPROPROC(c1,da)
```

UtilDBM2ORVarCom *Convert from DBM to OR variance components*

Description

UtilDBM2ORVarCom converts from DBM variance components to OR variance components

Usage

```
UtilDBM2ORVarCom(K, DBMVarCom)
```

Arguments

K	Total number of cases
DBMVarCom	DBM variance components, a data.frame containing VarR, VarC, VarTR, VarTC, VarRC and VarErr

Value

UtilDBM2ORVarCom returns the equivalent OR Variance components

Examples

```
DBMVarCom <- StSignificanceTesting(dataset02, FOM = "Wilcoxon", method = "DBM")$ANOVA$VarCom
UtilDBM2ORVarCom(114, DBMVarCom)

ORVarCom <- StSignificanceTesting(dataset02, FOM = "Wilcoxon", method = "OR")$ANOVA$VarCom
UtilOR2DBMVarCom(114, ORVarCom)
```

UtilFigureOfMerit *Calculate empirical figures of merit (FOMs) for specified dataset*

Description

Calculate the specified empirical figure of merit for each treatment-reader combination in the ROC, FROC, ROI or LROC dataset

Usage

```
UtilFigureOfMerit(dataset, FOM = "wAFROC", FPFValue = 0.2)
```

Arguments

dataset	The dataset to be analyzed, RJafroc-package
FOM	The figure of merit; the default is "wAFROC"
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.

Details

The allowed FOMs depend on the dataType field of the dataset object.

For dataset$descriptions$design = "SPLIT-PLOT-C"**, end-point based FOMs (e.g., "MaxLLF") are not allowed**. **For** dataset$descriptions$type = "ROC" **only** FOM = "Wilcoxon" **is allowed**. **For** dataset$descriptions$type = "FROC" **the following FOMs are allowed**:

- FOM = "AFROC1" (use only if zero normal cases)
- FOM = "AFROC"

- FOM = "wAFROC1" (use only if zero normal cases)
- FOM = "wAFROC" (the default)
- FOM = "HrAuc"
- FOM = "SongA1"
- FOM = "SongA2"
- FOM = "HrSe" (an example of an end-point based FOM)
- FOM = "HrSp" (another example)
- FOM = "MaxLLF" (do:)
- FOM = "MaxNLF" (do:)
- FOM = "MaxNLFAllCases" (do:)
- FOM = "ExpTrnsfmSp"

"MaxLLF", "MaxNLF" and "MaxNLFAllCases" correspond to ordinate, and abscissa, respectively, of the highest point on the FROC operating characteristic obtained by counting all the marks. The "ExpTrnsfmSp" FOM is described in the paper by Popescu. Given the large number of FOMs possible with FROC data, it is appropriate to make a recommendation: **it is recommended that one use the wAFROC FOM whenever possible.**

For dataType = "ROI" **dataset only** FOM = "ROI" **is allowed**.

For dataType = "LROC" dataset the following FOMs are allowed:

- FOM = "Wilcoxon" for ROC data inferred from LROC data
- FOM = "PCL" the probability of correct localization at specified FPFValue
- FOM = "ALROC" the area under the LROC from zero to specified FPFValue

FPFValue The FPF at which to evaluate PCL or ALROC; the default is 0.2; only needed for LROC data.

Value

An c(I,J) dataframe, where the row names are modalityID's of the treatments and column names are the readerID's of the readers.

References

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Chakraborty DP, Berbaum KS (2004) Observer studies involving detection and localization: modeling, analysis, and validation, Medical Physics, 31(8), 1–18.

Song T, Bandos AI, Rockette HE, Gur D (2008) On comparing methods for discriminating between actually negative and actually positive subjects with FROC type data, Medical Physics 35 1547–1558.

Popescu LM (2011) Nonparametric signal detectability evaluation using an exponential transformation of the FROC curve, Medical Physics, 38(10), 5690.

Obuchowski NA, Lieber ML, Powell KA (2000) Data Analysis for Detection and Localization of Multiple Abnormalities with Application to Mammography, Acad Radiol, 7:7 553–554.

Swensson RG (1996) Unified measurement of observer performance in detecting and localizing target objects on images, Med Phys 23:10, 1709–1725.

Examples

```
UtilFigureOfMerit(dataset02, FOM = "Wilcoxon") # ROC data
UtilFigureOfMerit(DfFroc2Roc(dataset01), FOM = "Wilcoxon") # FROC dataset, converted to ROC
UtilFigureOfMerit(dataset01) # FROC dataset, default wAFROC FOM
UtilFigureOfMerit(datasetCadLroc, FOM = "Wilcoxon") #LROC data
UtilFigureOfMerit(datasetCadLroc, FOM = "PCL") #LROC data
UtilFigureOfMerit(datasetCadLroc, FOM = "ALROC") #LROC data
UtilFigureOfMerit(datasetROI, FOM = "ROI") #ROI data
 # these are meant to illustrate conditions which will throw an error
## UtilFigureOfMerit(dataset02, FOM = "wAFROC") #error
## UtilFigureOfMerit(dataset01, FOM = "Wilcoxon") #error
```

UtilIntrinsic2PhysicalRSM

Convert from intrinsic to physical RSM parameters

Description

Convert **intrinsic** RSM parameters $lambda$ and nu correspond to the **physical** RSM parameters $lambda'$ and nu'. The physical parameters are more meaningful but they depend on mu. The intrinsic parameters are independent of mu. See book for details.

Usage

```
UtilIntrinsic2PhysicalRSM(mu, lambda, nu)
```

Arguments

mu	The mean of the Gaussian distribution for the ratings of latent LLs, i.e. continuous ratings of lesions that were found by the search mechanism ~ N(μ,1). The corresponding distribution for the ratings of latent NLs is N(0,1).
lambda	The Poisson *intrinsic* parameter, related to λ', the latter is the mean of the Poisson distribution of numbers of latent NLs (suspicious regions that do not correspond to actual lesions) per case.
nu	The *intrinsic* ν parameter; the corresponding *physical* parameter is the success probability of the binomial distribution of random numbers of latent LLs (suspicious regions that correspond to actual lesions) per diseased case, i.e., the chance that a lesion is "found".

Details

RSM is the Radiological Search Model described in the book. A latent mark becomes an actual mark if the corresponding rating exceeds the lowest reporting threshold $\zeta 1$. See also UtilPhysical2IntrinsicRSM.

Value

A list containing λ' and ν'

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449–3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
mu <- 2;lambda <- 20;nu <- 1.1512925
lambdaP <- UtilIntrinsic2PhysicalRSM(mu, lambda, nu)$lambdaP
nuP <- UtilIntrinsic2PhysicalRSM(mu, lambda, nu)$nuP
## note that the physical values are only constrained to be positive, but the physical variable nuP
## must obey 0 <= nuP <= 1
```

UtilLesionDistr *Lesion distribution of a dataset or as specified by a one-dimensional array*

Description

The lesion distribution for a dataset or lesions distribution specified as a one-dimensional array.

Usage

```
UtilLesionDistr(datasetOrLesDistr)
```

Arguments

`datasetOrLesDistr`
: A dataset or a one-dimensional array containing the lesion distribution. For example, c(0.1, 0.2, 0, 0.7) specifies 10 percent of diseased cases have one lesion, 20 percent have two lesions, 0 percent have 3 lesions and 70 percent have four lesions. See 3rd example below.

Details

Two characteristics of an FROC dataset, apart from the ratings, affect the FOM: the distribution of lesions per case and the distribution of lesion weights. This function addresses the lesions. The distribution of weights are addressed by UtilLesionWeightsDistr. `lesDistr` is a [1:nRow,2] array, where `nRow` is the number of **unique** values of lesions per case in the dataset, 1, 2, ..., etc. The first column of the array contains the number of lesions per case. The second column contains the corresponding fraction of diseased cases. See PlotRsmOperatingCharacteristics for a function that depends on `lesDistr`. See TBA Chapter00Vignette2 for more details. The underlying assumption is that lesion 1 is the same type across all diseased cases, lesion 2 is the same type across all diseased cases, etc. This allows assignment of weights independent of the case index. In the third example below, `relWeights` = [0.2, 0.4, 0.1, 0.3] means that on cases with one lesion the weight of lesion 1 is unity, on cases with two lesions the weight of the first lesion to that of the second lesion is in the ratio 0.2 : 0.4, i.e., lesion 2 is twice as important as lesion 1. On cases with 4 lesions the weights are in the ratio 0.2 : 0.4 : 0.1 : 0.3. There are no cases with 3 lesions in this example. Of course, on any case the weights sum to unity.

Value

lesDistr The lesion distribution array.

Examples

```
UtilLesionDistr (dataset01) # FROC dataset
UtilLesionDistr (dataset02) # ROC dataset
UtilLesionDistr (c(0.1, 0.2, 0, 0.7)) # We specify the distribution
```

UtilLesionWeightsDistr

Lesion weights distribution

Description

The lesion weights distribution of a dataset or the specified lesion weights distribution as a one-dimensional array..

Usage

```
UtilLesionWeightsDistr(datasetOrmaxLL, relWeights = 0)
```

Arguments

`datasetOrmaxLL`	A dataset, e.g., `dataset01`, or the maximum number of lesions in the dataset, `maxLL`.
`relWeights`	The relative weights of the lesions; a vector of length equal to `length(maxLL)`. The default is zero, in which case equal weights are assumed.

Details

Two characteristics of an FROC dataset, apart from the ratings, affect the FOM: the distribution of lesion per case and the distribution of lesion weights. This function addresses the weights. The distribution of lesions is addressed in UtilLesionDistr. `lesWghtDistr` is an [1:nRow,1:(maxLL+1)] array, where `nRow` is the number of **unique** values of lesions per case in the dataset. The first column enumerates the number of lesions per case, while the remaining columns contain the weights. Missing values are filled with `-Inf`. This parameter is not to be confused with the `lesionWeight` list member in an FROC dataset, which enumerates the weights of lesions on **individual** cases. See PlotRsmOperatingCharacteristics for a function that depends on `lesWghtDistr`. See TBA Chapter00Vignette2 for a fuller explanation. The underlying assumption is that lesion 1 is the same type across all diseased cases, lesion 2 is the same type across all diseased cases, ..., etc. This allows assignment of weights independent of the case index. In the third example below, 'relWeights' = [0.2, 0.4, 0.1, 0.3] means that on cases with one lesion the weight of lesion 1 is unity, on cases with two lesions the weight of the first lesion to that of the second lesion is in the ratio 0.2:0.4, i.e., lesion 2 is twice as important as lesion 1. On cases with 4 lesions the weights are in the ratio 0.2 : 0.4 : 0.1 : 0.3. There are no cases with 3 lesions in this example. Of course, on any case the weights sum to unity.

Value

lesWghtDistr The lesion weights distribution.

Examples

```
UtilLesionWeightsDistr (dataset01) # FROC data
UtilLesionWeightsDistr (dataset02) # ROC data

maxLL <- 4
relWeights <- c(0.2, 0.4, 0.1, 0.3)
UtilLesionWeightsDistr (maxLL, relWeights)
```

`UtilMeanSquares` *Calculate mean squares for factorial dataset*

Description

Calculates the mean squares used in the DBM and ORH methods for factorial dataset

Usage

```
UtilMeanSquares(dataset, FOM = "Wilcoxon", FPFValue = 0.2, method = "DBM")
```

Arguments

dataset	The dataset to be analyzed, see RJafroc-package.
FOM	The figure of merit to be used in the calculation. The default is "FOM_wAFROC". See UtilFigureOfMerit.
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
method	The method, in which the mean squares are calculated. The two valid choices are "DBM" (default) and "OR".

Details

For DBM method, msT,msTR,msTC,msTRC will not be available if the dataset contains only one treatment. Similarly, msR,msTR,msRC,msTRC will not be returned for single reader dataset. For ORH method, msT,msR,msTR will be returned for multiple reader multiple treatment dataset. msT is not available for single treatment dataset, and msR is not available for single reader dataset.

Value

A list containing all possible mean squares

Examples

```
UtilMeanSquares(dataset02, FOM = "Wilcoxon")
UtilMeanSquares(dataset05, FOM = "wAFROC", method = "OR")
```

UtilOR2DBMVarCom *Convert from OR to DBM variance components*

Description

UtilOR2DBMVarCom converts from OR to DBM variance components.

Usage

```
UtilOR2DBMVarCom(K, ORVarCom)
```

Arguments

K	Total number of cases
ORVarCom	OR variance components, a data.frame containing VarR, VarTR, Cov1, Cov2, Cov3 and Var

Value

UtilOR2DBMVarCom returns the equivalent DBM variance components

Examples

```
DBMVarCom <- StSignificanceTesting(dataset02, FOM = "Wilcoxon", method = "DBM")$ANOVA$VarCom
UtilDBM2ORVarCom(114, DBMVarCom)

ORVarCom <- StSignificanceTesting(dataset02, FOM = "Wilcoxon", method = "OR")$ANOVA$VarCom
UtilOR2DBMVarCom(114, ORVarCom)
```

UtilORVarComponentsFactorial

Utility for estimating Obuchowski-Rockette variance components for factorial datasets

---

Description

Utility for estimating Obuchowski-Rockette variance components for factorial datasets

Usage

```
UtilORVarComponentsFactorial(
  dataset,
  FOM,
  FPFValue = 0.2,
  covEstMethod = "jackknife",
  nBoots = 200,
  seed = NULL
)
```

Arguments

dataset	The factorial dataset object
FOM	The figure of merit
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.
covEstMethod	The covariance estimation method, "jackknife" (the default) or "bootstrap" or "DeLong" (DeLongt is applicable only for FOM = Wilcoxon).
nBoots	Only needed for bootstrap covariance estimation method. The number of bootstraps, defaults to 200.
seed	Only needed for the bootstrap covariance estimation method. The initial seed for the random number generator, the default is NULL, as if no seed has been specified.

Details

The variance components are obtained using StSignificanceTesting with method = "OR".

Value

A list object containing the following data.frames:

- foms: the figures of merit for different treatment-reader combinations
- TRanova: the OR treatment-reader ANOVA table
- VarCom: the OR variance-components Cov1, Cov2, Cov3, Var and correlations rho1, rho2 and rho3
- IndividualTrt: the individual treatment mean-squares, Var and Cov2 values
- IndividualRdr: the individual reader mean-squares, Var and Cov1 values

Examples

```
## use the default jackknife for covEstMethod
vc <- UtilORVarComponentsFactorial(dataset02, FOM = "Wilcoxon")
str(vc)

UtilORVarComponentsFactorial(dataset02, FOM = "Wilcoxon",
   covEstMethod = "bootstrap", nBoots = 2000, seed = 100)$VarCom

UtilORVarComponentsFactorial(dataset02, FOM = "Wilcoxon", covEstMethod = "DeLong")$VarCom
```

UtilOutputReport *Generate a text formatted report file or an Excel file*

Description

Generates a formatted report of the analysis and saves it to a text or an Excel file

Usage

```
UtilOutputReport(
  dataset,
  ReportFileBaseName = NULL,
  ReportFileExt = "txt",
  method = "DBM",
  FOM,
  alpha = 0.05,
  covEstMethod = "jackknife",
  nBoots = 200,
  sequentialNames = FALSE,
  overWrite = FALSE,
  analysisOption = "ALL"
)
```

Arguments

dataset	The dataset object to be analyzed (*not the file name*), see Dataset in RJafroc-package.
ReportFileBaseName	**This must be specified by the user.** The report file (text or Excel, as specified by option ReportFileExt) is then created **in the user's directory, not the RJafroc directory**. See README.md in the GitHub directory of this repository, the section on how to install the software, on how to create a user directory. This argument specifies the report file base name (i.e., without the extension) for the desired report; the default is NULL, in which case the system generates a temporary text file, whose very long name is displayed. However, the temp file is very hard to locate. This is so that the sofware passes CRAN checks, as writing to the project directory, or any of its subdirectories, is frowned upon.
ReportFileExt	The report file extension determines the type of output. txt, the default, for a text file, xlsx for an Excel file.
method	The significance testing method, "OR" or (the default) "DBM".
FOM	The figure of merit; see StSignificanceTesting.
alpha	See StSignificanceTesting; the default is 0.05.
covEstMethod	See StSignificanceTesting; only needed for method = "OR"; the default is "Jackknife".
nBoots	See StSignificanceTesting; only needed for "OR" analysis; the default is 200.
sequentialNames	A logical variable: if TRUE, consecutive integers (starting from 1) will be used as the treatment and reader IDs in the output report. Otherwise, treatment and reader IDs in the original dataset are used. This option is needed for aesthetics, as long names can mess up the output. The default is FALSE.
overWrite	A logical variable: if FALSE, a warning will be issued if the report file already exists and the program will wait until the user inputs "y" or "n" to determine whether to overwrite the existing file. If TRUE, the existing file will be silently overwritten. The default is FALSE.
analysisOption	"RRRC", "FRRC", "RRFC or "ALL"; see StSignificanceTesting.

Details

A formatted report of the data analysis is written to the output file in either text or Excel format.

Value

StResult The object returned by StSignificanceTesting.

Examples

```
 # text output is created in a temporary file
UtilOutputReport(dataset03, FOM = "Wilcoxon")
```

```
# Excel output is created in a temporary file
UtilOutputReport(dataset03, FOM = "Wilcoxon", ReportFileExt = "xlsx")
```

`UtilPhysical2IntrinsicRSM` *Convert from physical to intrinsic RSM parameters*

Description

Convert **physical** RSM parameters λ' and ν' to the **intrinsic** RSM parameters λ and ν. The physical parameters are more meaningful but they depend on μ. The intrinsic parameters are independent of μ. See book for details.

Usage

```
UtilPhysical2IntrinsicRSM(mu, lambdaP, nuP)
```

Arguments

`mu`	The mean of the Gaussian distribution for the ratings of latent LLs, i.e. continuous ratings of lesions that were found by the search mechanism ~ N(μ,1). The corresponding distribution for the ratings of latent NLs is N(0,1)
`lambdaP`	The Poisson *physical* parameter, which describes the distribution of random numbers of latent NLs (suspicious regions that do not correspond to actual lesions) per case; the mean of these random numbers asymptotically approaches lambdaP
`nuP`	The *physical* ν parameter; it is the success probability of the binomial distribution describing the random number of latent LLs (suspicious regions that correspond to actual lesions) per diseased case

Details

RSM is the Radiological Search Model described in the book. A latent mark becomes an actual mark if the corresponding rating exceeds the lowest reporting threshold zeta1. See also `UtilIntrinsic2PhysicalRSM`.

Value

A list containing λ and ν, the physical parameters

References

Chakraborty DP (2006) A search model and figure of merit for observer data acquired according to the free-response paradigm, Phys Med Biol 51, 3449-3462.

Chakraborty DP (2006) ROC Curves predicted by a model of visual search, Phys Med Biol 51, 3463–3482.

Chakraborty DP (2017) *Observer Performance Methods for Diagnostic Imaging - Foundations, Modeling, and Applications with R-Based Examples*, CRC Press, Boca Raton, FL.

Examples

```
mu <- 2;lambdaP <- 10;nuP <- 0.9
lambda <- UtilPhysical2IntrinsicRSM(mu, lambdaP, nuP)$lambda
nu <- UtilPhysical2IntrinsicRSM(mu, lambdaP, nuP)$nu
## note that the physical values are only constrained to be positive, e.g., nu is not constrained
## to be between 0 and one.
```

UtilPseudoValues *Pseudovalues for given dataset and FOM*

Description

Returns **centered** jackknife pseudovalues AND jackknife FOM values, for factorial OR split-plot-a OR split-plot-c study designs

Usage

```
UtilPseudoValues(dataset, FOM, FPFValue = 0.2)
```

Arguments

dataset	The dataset to be analyzed, see RJafroc-package; must be factorial, or split-plot-a or split-plot-c.
FOM	The figure of merit to be used in the calculation. The default is "FOM_wAFROC". See UtilFigureOfMerit.
FPFValue	Only needed for LROC data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.

Value

A list containing two arrays containing the pseudovalues and the jackknife FOM values of the datasets (a third returned value is for internal use).

Note

Each returned array has dimension c(I,J,K), where K depends on the FOM: K1 for FOMs that are based on normal cases only, K2 for FOMs that are based on abnormal cases only, and K for FOMs that are based on normal and abnormal cases.

Examples

```
UtilPseudoValues(dataset05, FOM = "wAFROC")$jkFomValues[1,1,1:10]
```

`UtilVarComponentsDBM` *Utility for Dorfman-Berbaum-Metz variance components*

Description

Utility for Dorfman-Berbaum-Metz variance components

Usage

```
UtilVarComponentsDBM(dataset, FOM, FPFValue = 0.2)
```

Arguments

`dataset`	The dataset object
`FOM`	The figure of merit
`FPFValue`	Only needed for `LROC` data **and** FOM = "PCL" or "ALROC"; where to evaluate a partial curve based figure of merit. The default is 0.2.

Value

A list object containing the variance components.

Examples

```
UtilVarComponentsDBM(dataset02, FOM = "Wilcoxon")
```

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